

GenCore version 5.1.8  
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OM protein - protein search, using sw model

Run on: May 21, 2006, 00:15:36 ; Search time 196 Seconds  
(without alignments)  
41.989 Million cell updates/sec

Title: US-09-857-000a-11

Perfect score: 91

Sequence: 1 RGGRLSYRRRFFSTSTGR 18

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 2589679 seqs, 457216429 residues

Total number of hits satisfying chosen parameters: 2589679

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 100 summaries

Database :

- A\_Geneseq\_8:\*
- 1: Geneseqp1980s:\*
  - 2: Geneseqp1990s:\*
  - 3: Geneseqp2000s:\*
  - 4: Geneseqp2001s:\*
  - 5: Geneseqp2002s:\*
  - 6: Geneseqp2003as:\*
  - 7: Geneseqp2003bs:\*
  - 8: Geneseqp2004s:\*
  - 9: Geneseqp2005s:\*
  - 10: Geneseqp2006s:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match %	Length	DB ID	Description
1	91	100.0	18	2	AAW99412
2	91	100.0	18	3	AAW93615
3	91	100.0	18	3	AAW93179
4	91	100.0	18	3	AAW93177
5	91	100.0	18	5	AAW48469
6	91	100.0	18	6	ABR43980
7	91	100.0	18	6	ABR84452
8	91	100.0	18	6	ABP70228
9	91	100.0	18	7	AAE38690
10	91	100.0	18	7	ADC42901
11	91	100.0	18	7	ADAE51568
12	91	100.0	18	7	ADG28016
13	91	100.0	18	7	ADL88652
14	91	100.0	18	8	ADG73831
15	91	100.0	18	8	ADH58869
16	91	100.0	18	8	ADH89792
17	91	100.0	18	8	ADN03484
18	91	100.0	18	8	ADR88701
19	91	100.0	18	8	ADU15732
20	91	100.0	18	9	ABEB28493
21	91	100.0	19	7	ADES1567
22	91	100.0	19	8	ADR88700
23	81	89.0	18	2	AAW99403

97 60 65.9 18 2 AAW18149 Aaw18149 Cationic,  
 98 60 65.9 18 2 AAW18147 Aaw18147 Cationic,  
 99 60 65.9 18 8 ADL18447 Adl18447 Antimicro  
 100 60 65.9 18 8 ADL18439 Adl18439 Antimicro

## ALIGNMENTS

RESULT 1  
 AAW99412  
 ID AAW99412 standard; peptide; 18 AA.  
 AC AAW99412;  
 XX  
 XX 08-JUN-1999 (first entry)  
 XX  
 XX Protegrin derivative peptide SM2196.  
 XX  
 XX Linear; protegrin; peptide antibiotic; beta-sheet; secondary structure;  
 KW disulphide bridge; antibody; ribozyme; antitumour agent; antiviral;  
 KW anti-inflammatory; mammal; cell membrane; passive transport; cytoplasm;  
 KW nucleus; blood-brain barrier.  
 XX  
 XX Synthetic.  
 XX  
 XX WO9907728-A2.  
 XX  
 XX 18-FEB-1999.  
 PD  
 XX 06-AUG-1998; 98WO-FR001757.  
 PP  
 XX 12-AUG-1997; 97FR-00010297.  
 PR  
 XX (SYNT-) SYNT:EM SA.  
 PA  
 XX Calas B, Grassy G, Chavanieu A, Kaczorek M;  
 PI  
 XX WPI; 1999-190034/16.  
 DR  
 XX Derivatives of antibiotic peptides lacking disulfide bridges - used as  
 PT carriers to deliver active agents into cells.  
 PT  
 XX Claim 7; Page 28; 37pp; French.  
 PS  
 XX This peptide represents a linear derivative of the protegrin family of  
 CC peptide antibiotics. Protegrin antibiotics form part of the peptide  
 CC antibiotic family which contain a beta-sheet secondary structure linked  
 CC by disulphide bridges. The new derivatives are linear and lack the  
 CC disulphide bridge. The novel derivatives are used to deliver active  
 CC agents to an organism, e.g. therapeutic proteins, antibodies (or their  
 CC fragments), nucleic acid, oligonucleotides, ribozymes, antitumour agents,  
 CC antivirals and anti-inflammatories, etc. The derivatives are non-toxic  
 CC and non-lytic but can cross mammalian cell membranes rapidly by a passive  
 CC mechanism, so can deliver active agents to cytoplasm and nucleus,  
 CC including crossing the blood-brain barrier  
 XX  
 SQ Sequence 18 AA;

Query Match 100.0%; Score 91; DB 2; Length 18;  
 Best Local Similarity 100.0%; Pred. No. 1.8e-07;  
 Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 RGGRLSYRRRFRSTGTGR 18  
 |||||  
 Db 1 RGGRLSYRRRFRSTGTGR 18

RESULT 2  
 AAY93615  
 ID AAY93615 standard; peptide; 18 AA.  
 XX  
 AC AAY93615;

XX 25-SEP-2000 (first entry)  
 DT  
 XX Peptide which may be linked to anticancer agents.  
 DE  
 XX Anticancer agent; cancer cell; resistance; P-glycoprotein pump; cancer.  
 KW  
 XX Unidentified.  
 OS  
 XX WO200032237-A1.  
 FN  
 XX 08-JUN-2000.  
 PD  
 XX 26-NOV-1999; 99WO-FR002939.  
 PF  
 XX 30-NOV-1998; 98FR-00015073.  
 PR  
 XX (SYNT-) SYNT:EM SA.  
 PA  
 XX Tamsamani J, Kaczorek M, Colin De Verdier A;  
 PI WPI; 2000-412166/35.  
 XX  
 DR New composition useful for cancer treatment and prevention, contains  
 PT anticancer agent and peptide vector that transports agent into cells.  
 PT  
 XX Disclosure; Page 8; 34pp; French.  
 PS  
 XX The specification describes a pharmaceutical composition, which comprises  
 CC at least one anticancer agent associated with at least one peptide that  
 CC can transport it into cancer cells and which inhibits development of  
 CC resistance to the anticancer agent. By using the peptide as a vector for  
 CC delivery of the anticancer agent, mechanisms that cause cancer cells to  
 CC become resistant to the agent, particularly the P-glycoprotein pump, are  
 CC avoided. Also, peptides are easily produced by chemical synthesis, can be  
 CC coupled easily to the agent, cross mammalian cell membranes rapidly by a  
 CC passive mechanism (no receptors required), and are non-toxic and non-  
 CC lytic. The compositions are used to treat cancer. The present sequence  
 CC represents a peptide which may be linked to the anticancer agents of the  
 CC invention  
 XX  
 XX Sequence 18 AA;

Query Match 100.0%; Score 91; DB 3; Length 18;  
 Best Local Similarity 100.0%; Pred. No. 1.8e-07;  
 Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 RGGRLSYRRRFRSTGTGR 18  
 |||||  
 Db 1 RGGRLSYRRRFRSTGTGR 18

RESULT 3  
 AAY93179  
 ID AAY93179 standard; peptide; 18 AA.  
 XX  
 AC AAY93179;

XX 06-DEC-2000 (first entry)  
 DT  
 XX Protegrin-like peptide antibiotic Dal-SynB1.  
 DE  
 XX Cytostatic; neurodegenerative; antidepressant; analgesic; antimicrobial;  
 KW blood-brain barrier; diagnostic; central nervous system; protegrin;  
 KW Antennapedia; tachyplesin; peptide antibiotic; Alzheimer's disease;  
 KW cancer; Parkinson's disease; depression; pain; meningitis; dalargin.  
 XX  
 XX Synthetic.

XX Key Location/Qualifiers  
 XX Cross-links 1  
 FT /note= "cross-links to a molecule of dalargin via a  
 FT disulphide linker"  
 FT

XX PN WO200032236-A1.  
XX PD 08-JUN-2000.  
XX PF 26-NOV-1999; 99WO-FR002938.  
XX PR 30-NOV-1998; 98FR-00015074.  
XX PA (SYNT-) SYNT:EM SA.  
XX PI Clair P, Kaczorek M, Tamsamani J;  
XX DR WPI; 2000-422871/36.  
XX PT Use of linear peptides as vectors for active ingredients, useful for  
XX diagnosis and treatment of central nervous system diseases, can transport  
XX agents passively across the blood-brain barrier.  
XX PS Example II; Page 20; 54pp; French.  
XX CC The invention relates to the use of linear peptides, coupled to an active  
XX agent, to prepare a composition able to cross the blood-brain barrier  
XX for diagnosis or treatment of disorders localised in the central nervous  
XX system. The linear peptide preferably has the formula: (a) X1- X16; (b);  
XX BXXXXXXBXXXXXB; or (c) BXXXXXXBXXXXXB, where: each of X1-X16 are  
XX amino acids (aa), of which 6-10 of them are hydrophobic and X6 must be  
XX Trp; each B is aa containing a side chain that includes a basic group;  
XX retro forms of (a)-(c) containing D- and/or L-form aa, or a fragment  
XX containing at least 5, preferably at least 7 consecutive aa from (a)-(c).  
XX Peptides able to cross the BBB include protegrins, Antennapedia,  
XX tachypleins, transportin, etc. Of these several families have cytolytic  
XX effects and are termed peptide antibiotics. They fall into 3 main  
XX categories based on their structure: (i) peptides with alpha-helices,  
XX e.g. cecropins and maganins; (ii) peptides with disulphide bond-linked  
XX beta-sheets, e.g. protegrin, tachypleins, defensins; (iii) peptides with  
XX no major structure but containing bends due to the presence of Pro  
XX residues, e.g. bactericins and PR39. The peptides of the invention fall  
XX into the peptide antibiotic categories defined above: (a)-peptides are  
XX based on the Antennapedia family peptides; (b)-peptides are based on  
XX protegrins; and (c)-peptides are based on tachypleins. This sequence  
XX represents a synthetic linear peptide designed on peptides able to cross  
XX the BBB and is conjugated to a daltargin molecule by a disulphide linker.  
XX Conjugates of the linear peptides and the active agent are particularly  
XX used to treat, prevent or diagnose brain cancer, Alzheimer's or  
XX Parkinson's diseases, depression, pain and meningitis, but also for  
XX studying drug behaviour in BBB models  
XX SQ Sequence 18 AA;  
Query Match 100.0%; Score 91; DB 3; Length 18;  
Best Local Similarity 100.0%; Pred. No. 1.8e-07; Mismatches 0; Gaps 0;  
Matches 18; Conservative 0; Indels 0; Gaps 0;  
QY 1 RGGRLSYRRRFFSTGTGR 18  
Db 1 RGGRLSYRRRFFSTGTGR 18  
RESULT 4  
AY93177  
ID AY93177 standard; peptide; 18 AA.  
AC AY93177;  
XX 06-DEC-2000 (first entry)  
XX Protegrin-like peptide antibiotic Doxo-SynB1.  
XX Cytostatic; neurodegenerative; antidepressant; analgesic; antimicrobial;  
XX blood-brain barrier; diagnostic; central nervous system; protegrin;  
XX Antennapedia; tachyplein; peptide antibiotic; Alzheimer's disease;

cancer; Parkinson's disease; depression; pain; meningitis.  
Synthetic.  
Key Location/Qualifiers  
Modified-site 1  
/note= "linked to doxorubicin via a succinate (-CO-(CH2)2  
-CO-) linker; optionally linked to benzylpenicillin by a  
glycoamide linker"  
WO200032236-A1.  
08-JUN-2000.  
26-NOV-1999; 99WO-FR002938.  
30-NOV-1998; 98FR-00015074.  
(SYNT-) SYNT:EM SA.  
Clair P, Kaczorek M, Tamsamani J;  
WPI; 2000-422871/36.  
Use of linear peptides as vectors for active ingredients, useful for  
diagnosis and treatment of central nervous system diseases, can transport  
agents passively across the blood-brain barrier.  
Example I; Page 13; 54pp; French.  
The invention relates to the use of linear peptides, coupled to an active  
agent, to prepare a composition able to cross the blood-brain barrier  
for diagnosis or treatment of disorders localised in the central nervous  
system. The linear peptide preferably has the formula: (a) X1- X16; (b);  
BXXXXXXBXXXXXB; or (c) BXXXXXXBXXXXXB, where: each of X1-X16 are  
amino acids (aa), of which 6-10 of them are hydrophobic and X6 must be  
Trp; each B is aa containing a side chain that includes a basic group;  
retro forms of (a)-(c) containing D- and/or L-form aa, or a fragment  
containing at least 5, preferably at least 7 consecutive aa from (a)-(c).  
Peptides able to cross the BBB include protegrins, Antennapedia,  
tachypleins, transportin, etc. Of these several families have cytolytic  
effects and are termed peptide antibiotics. They fall into 3 main  
categories based on their structure: (i) peptides with alpha-helices,  
e.g. cecropins and maganins; (ii) peptides with disulphide bond-linked  
beta-sheets, e.g. protegrin, tachypleins, defensins; (iii) peptides with  
no major structure but containing bends due to the presence of Pro  
residues, e.g. bactericins and PR39. The peptides of the invention fall  
into the peptide antibiotic categories defined above: (a)-peptides are  
based on the Antennapedia family peptides; (b)-peptides are based on  
protegrins; and (c)-peptides are based on tachypleins. This sequence  
represents a synthetic linear peptide designed on peptides able to cross  
the BBB and is conjugated to a daltargin molecule by a disulphide linker.  
Conjugates of the linear peptides and the active agent are particularly  
used to treat, prevent or diagnose brain cancer, Alzheimer's or  
Parkinson's diseases, depression, pain and meningitis, but also for  
studying drug behaviour in BBB models  
SQ Sequence 18 AA;  
Query Match 100.0%; Score 91; DB 3; Length 18;  
Best Local Similarity 100.0%; Pred. No. 1.8e-07; Mismatches 0; Gaps 0;  
Matches 18; Conservative 0; Indels 0; Gaps 0;  
QY 1 RGGRLSYRRRFFSTGTGR 18  
Db 1 RGGRLSYRRRFFSTGTGR 18  
RESULT 5  
AAW48469  
ID AAW48469 standard; peptide; 18 AA.

```
XX
AC AAM48469;
XX
DT 28-MAY-2002 (first entry)
XX
DE Antibiotic peptide SynB1.
XX
KW Amphipathic peptide; antibiotic peptide; carrier.
XX
OS Synthetic.
XX
PN WO200202595-A1.
XX
PD 10-JAN-2002.
XX
PF 03-JUL-2001; 2001WO-FR002129.
XX
PR 03-JUL-2000; 2000FR-00008633.
XX
PA (SYNT-) SYNT:EM SA.
XX
PI Drin G, Gomar J, Tamsamani J, Rees AR;
XX
DR WPI; 2002-241369/29.
XX
CC New amphipathic derivatives of antibiotic peptides, are useful for
PT delivering therapeutic and diagnostic agents to cells, provides efficient
PT transport across membranes.
XX
PS Claim 6; Page 23; 49pp; French.
XX
CC The present invention related to novel amphipathic antibiotic peptides.
CC The present sequence is one such peptide. The peptides are useful as
CC carriers for delivering attached active agents to cells, specifically to
CC a target site in cytoplasm or the nucleus, for therapeutic or diagnostic
CC use
XX
SQ Sequence 18 AA;
XX
Query Match 100.0%; Score 91; DB 5; Length 18;
Best Local Similarity 100.0%; Pred. NO. 1.8e-07;
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
OY 1 RGGRLSYRRRFFSTGTGR 18
Db |||||
1 RGGRLSYRRRFFSTGTGR 18
RESULT 6
ABR43980
ID ABR43980 standard; peptide; 18 AA.
XX
AC ABR43980;
XX
DT 11-AUG-2003 (first entry)
XX
DE Beta-stranded antibiotic peptide linear derivative.
XX
KW Antibiotic; antigen; immunostimulant; vaccine; immune response.
XX
OS Synthetic.
XX
PN WO2003033021-A1.
XX
PD 24-APR-2003.
XX
PF 15-OCT-2002; 2002WO-EP011500.
XX
PR 16-OCT-2001; 2001EP-00402671.
XX
PA (SYNT-) SYNT:EM SA.
XX
PI Johnson ME, Hamilton Day F, Kaczorek M, Tamsamani J;
XX
WPI; 2003-430304/40.
XX
New conjugates of antigens, which are coupled to a linear derivative of a
beta-stranded antibiotic peptide, useful for enhancing the immune
response of a mammal to an antigen, particularly useful in vaccination or
prophylaxis.
XX
Claim 7; Page 27; 57pp; English.
XX
The invention relates to a conjugate of an antigen, which is coupled to a
linear derivative of a beta-stranded antibiotic peptide. The conjugate is
useful for enhancing the immune response of a mammal to an antigen. The
conjugate is particularly useful in vaccination or prophylaxis. The
present sequence represents a linear derivative of a beta-stranded
antibiotic peptide
XX
SQ Sequence 18 AA;
XX
Query Match 100.0%; Score 91; DB 6; Length 18;
Best Local Similarity 100.0%; Pred No. 1.8e-07;
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
OY 1 RGGRLSYRRRFFSTGTGR 18
Db |||||
1 RGGRLSYRRRFFSTGTGR 18
RESULT 7
ABR84452
ID ABR84452 standard; peptide; 18 AA.
XX
AC ABR84452;
XX
DT 14-OCT-2003 (first entry)
XX
DE SynB1 peptide.
XX
KW Neuroprotective; Nootropic; Antiparkinsonian; Cytostatic; Anti-HIV;
KW Virucide; protegrin; tachyplesin; brain cancer; SynB1;
KW neurodegenerative disease; Alzheimer's disease; Parkinson's disease;
KW HIV infection.
XX
OS Unidentified.
XX
PN FR2829940-A1.
XX
PD 28-MAR-2003.
XX
PF 27-SEP-2001; 2001FR-00012442.
XX
PR 27-SEP-2001; 2001FR-00012442.
XX
PA (SYNT-) SYNT:EM SA.
XX
PI Tamsamani J, Roussele C, Rees AR;
XX
DR WPI; 2003-394101/37.
XX
New composition, useful for treating central nervous system diseases,
comprises an antibody linked to a linear peptide and is able to cross the
blood-brain barrier.
XX
Disclosure; Page 22; 25pp; French.
XX
The present invention relates to a composition (A), comprising at least
one antibody (Ab), or its fragment, linked to at least one linear peptide
(P) that is derived from protegrins or tachyplesins, or includes a
transduction domain. (A) is useful for diagnosis and treatment of
diseases of the central nervous system, e.g. neurodegenerative diseases
such as Alzheimer's and Parkinson's diseases, brain cancer or HIV
infection of the brain. The present peptide was used to illustrate the
invention
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XX SQ Sequence 18 AA;
Query Match 100.0%; Score 91; DB 6; Length 18;
Best Local Similarity 100.0%; Pred. No. 1.8e-07;
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 RGGRLSYRRRPFSTGTGR 18
Dd 1 RGGRLSYRRRPFSTGTGR 18
|||||

RESULT 8
ABP70228
ID ABP70228 standard; peptide; 18 AA.
XX AC ABP70228;
DT 07-APR-2003 (first entry)
XX DE Amino acid sequence of membrane translocating peptide SynB1.
XX KW Lipid-nucleic acid complex; polycation; targeting factor; gene therapy;
XX KW cancer; infection; immune deficiency; gene defect; genetic disease;
XX KW membrane translocating peptide.
XX OS Unidentified.
XX PN WO200288318-A2.
XX PD 07-NOV-2002.
XX PF 30-APR-2002; 2002WO-US013609.
XX PR 30-APR-2001; 2001US-0287786P.
XX PA (TARG-) TARGETED GENETICS CORP.
XX PA (EMER-) EMERALD GENE SYSTEMS LTD.
XX PI Harvie P, Paul R, Cudmore S, O'mahony DJ;
XX WPI; 2003-183837/18.
XX DE Lipid-nucleic acid complex useful for delivering a nucleic acid to a
XX PT cell, comprises compacted nucleic acid, polycation, targeting factor and
XX PT lipid, and does not comprise protamine or its salt.
XX PS Disclosure; Page 42; 259pp; English.
XX CC The specification describes a lipid-nucleic acid complex, comprising a
XX CC compacted nucleic acid, a polycation, a targeting factor and a lipid, but
XX CC not a protamine. The targeting factor increases cellular bioavailability
XX CC of the nucleic acid without interaction with a specific outer cell
XX CC surface membrane receptor. The mean diameter of the complex is greater
XX CC than 100 nm and less than 400 nm. The lipid-nucleic acid complex is
XX CC useful for delivering a nucleic acid to a cell in vivo, e.g. for gene
XX CC therapy. It reduces levels of inflammatory cytokines such as tumour
XX CC necrosis factor-alpha. The complex is useful for manufacturing a
XX CC medicament for treating or diagnosing a variety of diseases, conditions
XX CC or syndromes such as cancer, bacterial, viral or parasitic infections,
XX CC immune deficiencies, gene defects, and gene deficiencies (e.g. inherited
XX CC genetic diseases). The present sequence represents a membrane
XX CC translocating peptide, which is used as the targeting factor in lipid-
XX CC nucleic acid complexes of the invention
XX SQ Sequence 18 AA;
Query Match 100.0%; Score 91; DB 6; Length 18;
Best Local Similarity 100.0%; Pred. No. 1.8e-07;
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 RGGRLSYRRRPFSTGTGR 18
Dd 1 RGGRLSYRRRPFSTGTGR 18
|||||

RESULT 9
AAE38690
ID AAE38690 standard; peptide; 18 AA.
XX AC AAE38690;
DT 04-DEC-2003 (first entry)
XX DE SynB1 peptide.
XX KW Artificial transcription factor; DNA binding protein; ATF; ZFP; therapy;
XX KW zinc finger protein; crop protection; disease-resistant; transgenic;
XX KW transgenic plant.
XX OS Unidentified.
XX PN WO2003062455-A2.
XX PD 31-JUL-2003.
XX PF 23-JAN-2003; 2003WO-US002358.
XX PR 23-JAN-2002; 2002US-00057408.
XX PA (SYGN ) SYNGENTA PARTICIPATIONS AG.
XX PI Sera T;
XX WPI; 2003-646071/61.
XX DE Preparing an artificial transcription factor (ATF) capable of modulating
XX PT expression of a gene by interaction with a target site associated with
XX PT the gene, for treating plant disease, comprises preparing a combinatorial
XX PT library of ATFs.
XX PS Disclosure; Page 66; Opp; English.
XX CC The invention relates to a method of preparing artificial transcription
XX CC factor (ATF) capable of modulating expression of a gene by interaction
XX CC with a target site associated with the gene. The method comprises
XX CC preparing a combinatorial library of ATFs, each of the ATFs comprising a
XX CC DNA-binding domain and a transcriptional regulatory domain. The invention
XX CC also relates to DNA binding proteins comprising zinc finger domains and
XX CC particularly to the identification of a context-independent recognition
XX CC code to zinc finger domains. The methods are useful for treating disease
XX CC in a plant, for crop protection and for producing genetically transformed
XX CC disease-resistant plants. The present sequence is synB1 peptide used to
XX CC illustrate the method of the invention
XX SQ Sequence 18 AA;
Query Match 100.0%; Score 91; DB 7; Length 18;
Best Local Similarity 100.0%; Pred. No. 1.8e-07;
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 RGGRLSYRRRPFSTGTGR 18
Dd 1 RGGRLSYRRRPFSTGTGR 18
|||||

RESULT 10
ADC42901
ID ADC42901 standard; peptide; 18 AA.
XX AC ADC42901;
DT 18-DEC-2003 (first entry)
XX DE Syn B1 from Antennapedia homeodomain protein #SEQ ID 15.
XX DE

```

KW Zinc finger protein; ZFP; artificial zinc finger protein; AFP;  
 KW nuclear envelope; nuclear lamina; heterochromatin; GCL protein;  
 KW gene expression; cytokine; interleukin; oncogene; angiogenesis factor;  
 KW drug resistance protein; growth factor; tumour suppressor; DNA binding.  
 XX  
 OS Synthetic.  
 XX  
 PN WO2003062447-A2.  
 XX  
 XX 31-JUL-2003.  
 XX  
 XX 17-JAN-2003; 2003WO-US001529.  
 XX  
 XX 18-JAN-2002; 2002US-0350163P.  
 PR 23-JAN-2002; 2002US-035115P.  
 XX  
 XX (SYGN ) SYNGENTA PARTICIPATIONS AG.  
 PA  
 XX Sera T;  
 XX  
 XX WPI; 2003-803624/75.  
 DR  
 XX  
 XX Nucleic acid target-specific chimeric proteins comprising a nuclear-  
 PT envelope and/or nuclear lamina binding domain and a DNA binding domain  
 PT used in methods to repress or down-regulate expression of selected genes.  
 PT  
 XX  
 XX Disclosure; SEQ ID NO 15; 60pp; English.  
 PS  
 XX  
 CC The invention relates to a nucleic acid target-specific chimeric protein  
 CC comprising one or more first domains capable of specifically binding a  
 CC nucleotide sequence associated with a target gene, and one or more second  
 CC domains capable to associating with the nuclear periphery, where at least  
 CC one of the first domains is heterologous with respect to at least one of  
 CC the second domains. The one or more first domains comprise at least three  
 CC zinc finger proteins (ZFP's) or artificial zinc finger proteins (AZP's)  
 CC directly joined to one another. The one or more second domains directly  
 CC or indirectly associate with or bind to the nuclear envelope, the nuclear  
 CC lamina, heterochromatin or any combinations of these. One of the second  
 CC domains is a GCL protein or a binding moiety of a GCL protein. The  
 CC chimeric proteins of the invention and the nucleic acids encoding them  
 CC can be used to repress, down regulate or decrease gene expression of a  
 CC target gene in an eukaryotic organism, including yeast animals and plants  
 CC and may encode a cytokine, an interleukin, an oncogene, an angiogenesis  
 CC factor, an anti-angiogenesis factor, a drug resistance protein, a growth  
 CC factor or a tumour suppressor. The chimeric proteins can be used to  
 CC inhibit the expression of a disease-associated gene. The invention  
 CC provides a new method of transcriptional repression of genes. Previously  
 CC used transcription factors have limited utility or are limited to a set  
 CC of closely related target sequences. The zinc finger proteins of the  
 CC invention are DNA binding proteins with predetermined sequence  
 CC specificity for unique target sequences in a large complex genome. An  
 CC example from the invention demonstrates the repression of the human  
 CC vascular endothelial growth factor A (VEGF-A) gene. The current sequence  
 CC represents Syn B1 from the Antennapedia homeodomain protein. This peptide  
 CC is capable of carrying substances across the blood brain barrier.  
 XX  
 SQ Sequence 18 AA;  
 Query Match 100.0%; Score 91; DB 7; Length 18;  
 Best Local Similarity 100.0%; Pred. No. 1.8e-07;  
 Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 Qy 1 RGGRLSYRRRFTSTGCR 18  
 |||||  
 Db 1 RGGRLSYRRRFTSTGCR 18  
 |||||  
 RESULT 11  
 ADE51568  
 ID ADE51568 standard; peptide; 18 AA.  
 XX  
 AC ADE51568;  
 XX

DT 29-JAN-2004 (first entry)  
 XX  
 DE Peptide #6 to transport cyclosporin compound across blood brain barrier.  
 XX  
 KW neuroprotective; cerebroprotective; vulnery; hemostatic;  
 KW anticonvulsant; neuroleptic; thrombolytic; anticoagulant; vasotropic;  
 KW nootropic; antiparkinsonian; cytostatic; antidiabetic; antibacterial;  
 KW anti-HIV; ophthalmological; antiinflammatory; virucide; protozoacide;  
 KW immunosuppressive; dermatological; antithyroid; antidote; antirheumatic;  
 KW antiarthritic; antipsoriatic; endocrine-general; cyclophilin inhibitor;  
 KW calcineurin inhibitor;  
 KW neurotoxic calcium-dependent enzyme cascade blocker;  
 KW mitochondrial stabilizer; cyclosporin; transporter; blood-brain barrier.  
 XX  
 OS Synthetic.  
 XX  
 PN WO2003070755-A2.  
 XX  
 XX 28-AUG-2003.  
 XX  
 XX 24-FEB-2003; 2003WO-FR000591.  
 PF  
 XX 22-FEB-2002; 2002FR-00002299.  
 PR  
 XX (SYNT-) SYNT:EM.  
 XX (MAAS-) MAAS BIOLAB LLC.  
 PA  
 XX Mouchet P, Rees AR, Elmer E, Keep MF;  
 PI  
 XX WPI; 2003-712609/67.  
 DR  
 XX  
 XX New cyclosporin derivatives, containing bonded peptide vector for  
 PT crossing blood-brain barrier, used for treating cerebral disorders such  
 PT as neurodegenerative diseases, cerebral trauma or cerebrovascular  
 PT accidents.  
 PT  
 XX Disclosure; SEQ ID NO 6; 77pp; French.  
 PS  
 XX  
 CC The invention relates novel cyclosporin compounds (I) comprise at least  
 CC one cyclosporin molecule (II) and at least one peptide vector (III)  
 CC capable of transporting (I) across the blood-brain barrier. (I) are used  
 CC for the treatment or prevention of: (i) acute neurological disorders,  
 CC e.g. due to traumatic cerebral lesions, spinal cord lesions, exposure to  
 CC radiation, chemotherapy, epilepsy, schizophrenia, cerebral or spinal  
 CC surgery, cerebrovascular accidents, embolic cerebrovascular accident,  
 CC global cerebral ischemia, ruptured aneurysms, subarachnoid hemorrhage,  
 CC vascular spasms or hemorrhagic vascular accidents; (ii) neurodegenerative  
 CC diseases selected from Alzheimer's disease, Parkinson's disease,  
 CC Huntington's disease, Down syndrome, Charcot disease, spino-muscular  
 CC atrophy, bulbar paralysis, schizophrenia, Tourette syndrome, diffuse  
 CC cerebrotical atrophy, Lewy body dementia, mesolimbocortical dementia,  
 CC thalamic degeneration, Pick disease, multisystem dementia, cortico-  
 CC striato-spinal degeneration, Shy-Drager syndrome, Richardson-Steale-  
 CC Olzewski syndrome, Parkinson-amyotrophic lateral sclerosis-Guam dementia  
 CC complex, post-polio syndrome, olivo-cerebellar atrophy, Friedreich  
 CC ataxia, paraneoplastic syndrome, traumatic chronic encephalopathy  
 CC boxer's dementia), Wilson disease, Menke disease, Tay-Sachs gangliosidosis,  
 CC Krabbe disease, peripheral neuropathy, diabetic neuropathy or aging;  
 CC (iii) prion diseases, such as Creutzfeldt Jacob disease (CJD), atypic CJD,  
 CC kuru, scrapie or bovine spongiform encephalitis; (iv) retroviral  
 CC diseases, e.g. AIDS dementia, AIDS myelopathy, AIDS peripheral neuropathy  
 CC or tropical paraparesis; (v) visual and retinal disorders, e.g. glaucoma-  
 CC related degeneration, macular degeneration, diabetic degeneration,  
 CC diabetic retinopathy, degeneration-related inflammation, detached retina,  
 CC optical neuritis, optic nerve lesions, optical chiasm or optical tractus  
 CC and retinal lesions caused by photons, trauma, ischemia or elevated  
 CC intracranial pressure; (vi) vital and bacterial diseases associated with  
 CC encephalopathy, including herpetic, equine, post-vaccination, Japanese or  
 CC Nile encephalitis, meningitis, rabies, poliomyelitis, progressive  
 CC multifocal leuko-encephalopathy, subacute sclerotic panencephalitis,  
 CC cerebral malaria, Lyme disease or neurosyphilis; (vii) immunological  
 CC diseases, e.g. plaque sclerosis, Guillain-Barre syndrome, lupus  
 CC erythematosus or Graves disease; (viii) the effects of neurotoxins,

CC including aminoglycosides, chlorinated hydrocarbons, organophosphates,  
 CC insecticides, herbicides, paraquat, nerve gas, 1-methyl-4-phenyl-1,2,3,6-  
 CC tetrahydropyridine, rotenone, cyanide, carbon monoxide, methanol,  
 CC ethanol, mercury, arsenic, chemotherapeutic agents (e.g. methotrexate,  
 CC mercaptopurine, fluorouracil, nitrosoureas, hydroxyurea, cisplatin,  
 CC carboplatin, daunorubicin, etoposide, vincristine, vinblastine, taxol (or  
 CC derivatives) or cyclophosphamide) or corticosteroids; (ix) metabolic  
 CC encephalopathy, e.g. hepatic or uremic encephalopathy; (x) conditions  
 CC requiring induction of a non-immune state, e.g. transplantation of  
 CC organs, tissues or cells or immune or autoimmune diseases such as  
 CC rheumatoid arthritis, eczema, psoriasis or alopecia; or (xi)  
 CC chemotherapy-resistant tumors. This sequence is an example of the peptide  
 CC part of the compound.  
 XX  
 SQ Sequence 18 AA;

Query Match 100.0%; Score 91; DB 7; Length 18;  
 Best Local Similarity 100.0%; Pred. No. 1.8e-07;  
 Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 RGGRLSYRRRFFSTGTGR 18  
 |||||  
 DB 1 RGGRLSYRRRFFSTGTGR 18

RESULT 12  
 ADG28016  
 ID ADG28016 standard; peptide; 18 AA.  
 AC  
 AC ADG28016;  
 XX  
 DT 26-FEB-2004 (first entry)  
 DE  
 DE Protegrin/porcine leukocyte SynBl membrane fusion sequence.  
 XX  
 KW fusion protein; cold shock domain; membrane translocation sequence; CspA;  
 KW CspB; CspC; CspD; rpi S1 binding domain; eukaryotic Y-box protein;  
 KW DNA binding protein B; DBPB; DBPA; EPE-1; MRNP3; MRNP4; FRG Y1;  
 KW nuclease-sensitive element binding protein 1; NSEP 1;  
 KW DNA condensation domain; DNA binding domain; SPKR;  
 KW nuclear localisation sequence; NLS; protein purification tagged sequence;  
 KW gene delivery; protegrin; porcine leukocyte; synBl;  
 KW membrane fusion sequence.  
 XX  
 OS Synthetic.  
 XX  
 PN US2003211590-A1.  
 XX  
 PD 13-NOV-2003.  
 XX  
 PF 13-MAY-2002; 2002US-00144549.  
 XX  
 PR 13-MAY-2002; 2002US-00144549.  
 XX

PA (HMUP/) HWU P L.  
 XX  
 PI HWU PL;  
 XX  
 XX WPI; 2003-901590/82.  
 DR  
 XX  
 XX New fusion protein comprising a cold shock domain, and a membrane  
 PT translocation sequence, useful for delivering DNAs and RNAs to in vivo  
 PT cells for gene delivery.  
 XX

PS Claim 9; SEQ ID NO 17; 24pp; English.  
 XX  
 XX The invention describes a fusion protein for delivery of a desired  
 CC molecule into cells or nuclei, comprising a cold shock domain, its  
 CC homologue and functional derivative, and a membrane translocation  
 CC sequence or its functional equivalent peptides and/or derivatives. The  
 CC fusion protein comprises a cold shock domain that is selected from CspA,  
 CC CspB, CspC, CspD, rpi S1 binding domain, eukaryotic Y-box proteins, DNA  
 CC binding protein B (DBPB), DBPA, EPE-1, MRNP3, MRNP4, FRG Y1 and nuclease-

CC sensitive element binding protein 1 (NSEP 1). The functional equivalent  
 CC derivative of cold shock protein is modified by inserting into the cold  
 CC shock domain with a DNA condensation domain or a DNA binding domain. The  
 CC DNA condensation or binding domain is selected from DNA condensation  
 CC domain (SPKR) 3-4 and the positive charge nuclear localisation sequences  
 CC (NLS+). The membrane transduction sequence is protein transduction domain  
 CC (PTD) or membrane fusion sequence. The fusion protein further comprises a  
 CC protein purification tagged sequence selected from HA, GST, and His6 tag.  
 CC The fusion protein is useful for delivering DNAs and RNAs to in vivo  
 CC cells for gene delivery, or for delivering nucleic acids to an embryo or  
 CC to a living animal for the production of transgenic animal. This is the  
 CC amino acid sequence of protegrin/porcine leukocyte derived synBl membrane  
 CC fusion sequence.  
 XX  
 SQ Sequence 18 AA;

Query Match 100.0%; Score 91; DB 7; Length 18;  
 Best Local Similarity 100.0%; Pred. No. 1.8e-07;  
 Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 RGGRLSYRRRFFSTGTGR 18  
 |||||  
 DB 1 RGGRLSYRRRFFSTGTGR 18

RESULT 13  
 ADL88652  
 ID ADL88652 standard; peptide; 18 AA.  
 XX  
 AC ADL88652;  
 XX  
 DT 20-MAY-2004 (first entry)  
 DE  
 DE SynBl membrane fusion sequence peptide.  
 XX  
 KW fusion protein; cold shock domain; membrane translocation; gene therapy;  
 KW transgenic; membrane fusion; SynBl.  
 XX  
 OS Unidentified.  
 XX  
 PN JP2004035409-A.  
 XX  
 PD 05-FEB-2004.  
 XX  
 PF 15-MAY-2002; 2002JP-00140441.  
 XX  
 PR 13-MAY-2002; 2002US-00144549.  
 XX

PA (GENE-) GENESHUTTLE BIOPHARM INC.  
 XX  
 PI HWU PL;  
 XX  
 XX WPI; 2003-901590/82.  
 DR  
 XX  
 XX New fusion protein comprising a cold shock domain, and a membrane  
 PT translocation sequence, useful for delivering DNAs and RNAs to in vivo  
 PT cells for gene delivery.  
 XX

PS Claim 9; SEQ ID NO 15; 53pp; Japanese.

XX  
 XX The invention relates to a novel fusion protein for delivery of a desired  
 CC molecule into cells or nuclei comprising a cold shock domain, its  
 CC homologue and functional derivative and a membrane translocation sequence  
 CC or its functionally equivalent peptides and/or derivatives. The fusion  
 CC protein of the invention may be useful for delivering DNAs and RNAs to in  
 CC vivo cells for gene therapy or for delivering nucleic acids to an embryo  
 CC or to a living animal for the production of transgenic animals. The  
 CC current sequence is that of a membrane fusion sequence peptide of the  
 CC invention.  
 XX

SQ Sequence 18 AA;

Query Match 100.0%; Score 91; DB 7; Length 18;

```
Best Local Similarity 100.0%; Pred. No. 1.8e-07;
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 RGGRLSYRRRFFSTSTGR 18
Db 1 RGGRLSYRRRFFSTSTGR 18

RESULT 14
ADG73831
ID ADG73831 standard; peptide; 18 AA.
XX AC ADG73831;
XX 11-MAR-2004 (first entry)
XX Membrane-penetrating peptide SynB1.
DE SynB1; drug delivery; nanoparticle.
XX Unidentified.
XX EP1362599-A2.
PN EP1362599-A2.
XX 19-NOV-2003.
XX 28-JUN-2002; 2002EP-00254597.
XX 17-MAY-2002; 2002KR-00027328.
XX (PACI-) PACIFIC CORP.
XX Chang IS, Park JY, Nam YS, Han SH;
PI WPI; 2004-055143/06.
DR Conjugate of biodegradable aliphatic polyester-based polymer with Tat(49-
PT 57) peptide or peptide chain containing the Tat(49-57) peptide, useful
PT for manufacturing nanoparticle with enhanced intracellular permeability.
XX Disclosure; SEQ ID NO 3; 18pp; English.
XX The present sequence is that of SynB1, a membrane-permeable peptide of
CC protegrins. The peptide has been examined previously as a means for
CC improving drug delivery through the blood-brain barrier. The present
CC invention provides a conjugate of a biodegradable aliphatic polyester-
CC based polymer and the membrane-permeable Tat49-57 peptide ADG73829 from
CC HIV-1, or a peptide including Tat49-57. The Tat49-57 peptide (A) and the
CC biodegradable aliphatic polyester-based polymer (B) are constituted as A-
CC B type or A-B-A type. The conjugate is used to manufacture nanoparticles
CC of average diameter not more than 1,000 nm. These nanoparticles can be
CC used as a drug delivery system with an improved bioavailability in vivo.
XX Sequence 18 AA;

Query Match 100.0%; Score 91; DB 8; Length 18;
Best Local Similarity 100.0%; Pred. No. 1.8e-07;
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 RGGRLSYRRRFFSTSTGR 18
Db 1 RGGRLSYRRRFFSTSTGR 18

RESULT 16
ADH89792
ID ADH89792 standard; peptide; 18 AA.
XX ADH89792;
AC ADH89792;
XX 22-APR-2004 (first entry)
XX Cell penetrating peptide (CPP) identification method-related peptide 106.
DE cell-penetrating peptide; CPP; bulk property value Z-E; Z-E1; Z-E2; Z-E3;
XX Z-E4; Z-E5; antidiabetic; neuroprotective; nootropic; antiparkinsonian;
KW cardiant; cytostatic; tranquiliser; immunosuppressive; antidepressant;
KW anticonvulsant; antiinflammatory; analgesic; neuroleptic;
KW ophthalmological; antiulcer; cell-penetration; infectious disease;
KW diabetes type I; diabetes type II; Alzheimer's disease;
KW Parkinson's disease; cancer; prion disease; cardiovascular disease;
KW signal transduction.
XX Unidentified.
OS WO2003106491-A2.
XX 24-DEC-2003.
XX 18-JUN-2003; 2003WO-IB003163.
XX
```

PR 18-JUN-2002; 2002SE-00001863.  
PR 25-JUN-2002; 2002US-0391788P.  
XX (CEPE-) CEPEP AB.  
XX  
XX Haelbrink M, Pooga M, Metsis M, Kogerman P, Valkna A, Meikas A;  
PI Lindgren M, Graeslund A, Eriksson G, Oestensson CG, Budhina M;  
PI Zorko M, Elmquist A, Soomets U, Lundberg P, Jaerver P, Saar K;  
PI El-Andalousi S, Kilk K, Langel U;  
XX WPI; 2004-090832/09.  
XX  
XX Predicting, designing, detecting, and/or verifying novel cell-penetrating  
PT peptide based on assessment of bulk property value of sequences of cell-  
PT penetrating peptide.  
XX  
XX Example 11; Page 17; 148pp; English.  
XX  
XX This invention relates to a novel method of identifying, designing,  
CC detecting, and/or verifying novel cell-penetrating peptide (CPP) based on  
CC assessment of bulk property value Z-B of sequences of CPP comprising 5 or  
CC more individual average interval values Z-E1, Z-E2, Z-E3, Z-E4 and Z-E5,  
CC where Z-E1, Z-E2, Z-E3, Z-E4 and Z-E5 are average values of the  
CC respective descriptor values for the residues in the amino acid sequence.  
CC The invention may be useful for the development of compounds with an  
CC antidiabetic, neuroprotective, nootropic, antiparkinsonian, cardiant,  
CC cytosstatic, tranquiliser, immunosuppressive, antidepressant,  
CC anticonvulsant, antiinflammatory, analgesic, neuroleptic,  
CC ophthalmological or anticancer activity as a stimulator of cell-  
CC penetration. The method of the invention is useful for identifying a cell-  
CC -penetrating peptide or protein and/or a cell-penetrating fragment of a  
CC peptide or protein. In addition, the invention may be useful for checking  
CC cellular penetration properties of a peptide, for producing a cell-  
CC penetrating and functional protein-mimicking peptide and for de novo  
CC design and production of an artificial cell-penetrating and/or and  
CC artificial cell-penetrating and functional protein-mimicking peptide.  
CC Compositions developed within the scope of the present invention may be  
CC useful for treating infectious diseases, diabetes type I, diabetes type  
CC II, Alzheimer's disease, Parkinson's diseases, cancer, prion disease,  
CC cardiovascular disease or disorders resulting from perturbed signal  
CC transduction. The method of the invention is fast, efficient and reliable  
CC for identifying, detecting, designing CPPs and for screening cellular  
CC uptake of a broad variety of CPPs in vitro and in vivo. The present  
CC sequence is that of a peptide which was used in the exemplification of  
CC the invention.  
XX  
XX SQ Sequence 18 AA;  
Query Match 100.0%; Score 91; DB 8; Length 18;  
Best Local Similarity 100.0%; Pred. No. 1.8e-07;  
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
Qy 1 RGGRLSYRRRPFSTGTGR 18  
Db 1 RGGRLSYRRRPFSTGTGR 18  
RESULT 17  
ADN03484  
ID ADN03484 standard; peptide; 18 AA.  
XX  
XX ADN03484;  
XX  
XX 01-JUL-2004 (first entry)  
XX Beta-stranded protegrin peptide linear deriative #7.  
DB Beta-stranded antibiotic peptide; immune response; therapy; vaccine;  
XX protegrin.  
KW  
KW Unidentified.  
XX  
XX US2004072340-A1.  
PN

XX 15-APR-2004.  
XX PD  
XX PF 15-OCT-2002; 2002US-00270010.  
XX PR 15-OCT-2002; 2002US-00270010.  
XX (JOHN/) JOHNSON M E.  
PA (DAYF/) HAMILTON DAY F.  
PA (KACZ/) KACZOREK M.  
PA (TEMS/) TEMSAMANI J.  
XX Johnson ME, Hamilton Day F, Kaczorek M, Tamsamani J;  
PI WPI; 2004-328576/30.  
XX  
XX New conjugates of an antigen coupled to a linear derivative of a beta-  
PT stranded antibiotic peptide, useful for enhancing the immune response of  
PT a mammal to an antigen.  
XX  
XX Claim 7; SEQ ID NO 10; 21pp; English.  
XX  
XX The present invention relates to conjugates of an antigen coupled to a  
CC linear derivative of a beta-stranded antibiotic peptide. The invention is  
CC useful for enhancing the immune response of a mammal to an antigen. The  
CC invention is also useful in the production of vaccines. The present  
CC sequence is a beta-stranded protegrin (antibiotic) peptide linear  
CC derivative.  
XX  
XX SQ Sequence 18 AA;  
Query Match 100.0%; Score 91; DB 8; Length 18;  
Best Local Similarity 100.0%; Pred. No. 1.8e-07;  
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
Qy 1 RGGRLSYRRRPFSTGTGR 18  
Db 1 RGGRLSYRRRPFSTGTGR 18  
RESULT 18  
ADR88701  
ID ADR88701 standard; peptide; 18 AA.  
XX  
XX ADR88701;  
XX  
XX 18-NOV-2004 (first entry)  
XX  
XX Amino acid sequence of a peptide designated SynB1.  
XX disease treatment; active substance transport; bioavailability; SynB1;  
XX cyclosporin A.  
XX Unidentified.  
XX  
XX FR2851471-A1.  
XX  
XX 27-AUG-2004.  
XX  
XX 24-FEB-2003; 2003FR-00002242.  
XX  
XX 24-FEB-2003; 2003FR-00002242.  
XX (SYNT-) SYNT:EM SA.  
XX  
XX Rees AR, Mouchet P;  
PI WPI; 2004-627939/61.  
XX  
XX Compound comprising active agent coupled to vector through a linker,  
PT useful in human or veterinary medicine, where the linker includes a  
PT hydroxyproline residue.  
XX

PS Disclosure; SEQ ID NO 6; 65pp; French.

XX The specification describes a compound comprising at least one active

CC substance and at least one vector, connected by a linker that includes a

CC hydroxyproline residue. The linker is of a formula given in the

CC specification. The vector modifies the physicochemical or pharmacokinetic

CC properties of the active substance. The active substance is a protein,

CC (poly)peptide, antibody (or fragment), nucleic acid, oligonucleotide,

CC ribozyme, or a chemical for treatment or prevention of human or animal

CC disease, e.g. an antitumour or antiviral agent. Alternatively, it is a

CC radioactive or coloured material, or some other substance suitable as

CC indicator of metabolism or disease. Compounds of the invention are used

CC for treatment, prevention and diagnosis of disease in human or veterinary

CC medicine. They facilitate transport of the active substance across

CC biological barriers and its penetration into cells, and they also modify

CC the bioavailability or solubility of active substances. The present

CC sequence represents a peptide designated SynBl. SynBl was joined to

CC cyclosporin A via a linker to produce exemplary compounds of the

CC invention.

XX Sequence 18 AA;

SEQ

Query Match 100.0%; Score 91; DB 8; Length 18;

Best Local Similarity 100.0%; Pred. No. 1.8e-07;

Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 RGGRLSYRRRFFSTGTGR 18

DB 1 RGGRLSYRRRFFSTGTGR 18

RESULT 19

ADU15732

ID ADU15732 standard; peptide; 18 AA.

XX

AC ADU15732;

XX

DT 13-JAN-2005 (first entry)

XX

DE MUC1-PDZ domain binding inhibitor transmembrane transporter peptide #20.

XX

KW cytoplasmic domain; MUC1; PDZ domain; transmembrane transporter.

XX

OS Unidentified.

XX

PN WO2004092339-A2.

XX

PD 28-OCT-2004.

XX

PF 12-APR-2004; 2004WO-US011195.

XX

PR 11-APR-2003; 2003US-0462111P.

XX

PR 02-MAY-2003; 2003US-0467728P.

XX

PR 04-JUN-2003; 2003US-0475595P.

XX

PR 11-SEP-2003; 2003US-0502111P.

XX

PR 21-NOV-2003; 2003US-0524188P.

XX

PA (ILEX-) ILEX PROD INC.

XX

PA (ARBO-) ARBOR VITA CORP.

XX

PA (DAND ) DANA FARBER CANCER INST.

XX

PI Belmares MP, Lu PS, Garman JD, Jecminek AA, Kharbanda S, Agata N;

XX

PI Kufe DW;

XX

XX WPI; 2004-766852/75.

XX

XX Inhibiting the binding of the cytoplasmic domain of MUC1 to a PDZ domain,

XX comprises contacting the PDZ domain with an agent that competes with the

XX binding of the C-terminal region of the cytoplasmic domain of MUC1 with

XX the PDZ domain.

XX

PS Claim 9; SEQ ID NO 116; 141pp; English.

XX

CC The invention relates to a method of inhibiting the binding of the

CC cytoplasmic domain of MUC1 to a PDZ domain, by contacting the PDZ domain

CC with an effective amount of an agent that competes with the binding of

CC the C-terminal region of the cytoplasmic domain of MUC1 with the PDZ

CC domain. The PDZ domain is ZO-1 d2, SIP1 d1, LIM MYSTIQUE, AIPC, KIAA0751,

CC MAST2, PRIL-16 d1, GRIP2 d5, SITAC 18, NSP or KIAA1526 d1. The agent that

CC competes with binding of the C-terminal region of cytoplasmic domain of

CC MUC1 with the PDZ domain is a peptide of the formula (I): X1-aa2-aal-aa0,

CC where aa0 is a hydrophobic aliphatic amino acid residue or a hydrophobic

CC aromatic amino acid residue; aa2 is a hydrophobic aliphatic amino acid

CC residue, hydrophobic aromatic amino acid residue, polar amino acid

CC residue, basic amino acid residue or an acidic amino acid residue; aal is

CC any amino acid residue; and X1 is a sequence of 0-50 amino acid residues.

CC Preferably aa2-aal-aa0 is selected from SEQ ID NO: 1-40 (ADU15617-

CC ADU15656) and X1 may be selected from SEQ ID NO: 41-94 (ADU15657-

CC ADU15710). The method is useful for inhibiting the binding of the

CC cytoplasmic domain of MUC1 to a PDZ domain. The amino terminal of the X1

CC peptide may also contain a transmembrane transporter peptide. The

CC transporter sequence may be selected from SEQ ID NO: 97-127 (ADU15713-

CC ADU15743). This peptide is derived from a pegelin protein.

XX

SEQ

Query Match 100.0%; Score 91; DB 8; Length 18;

Best Local Similarity 100.0%; Pred. No. 1.8e-07;

Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 RGGRLSYRRRFFSTGTGR 18

DB 1 RGGRLSYRRRFFSTGTGR 18

RESULT 20

AE28493

ID AEB28493 standard; peptide; 18 AA.

XX

AC AEB28493;

XX

DT 22-SEP-2005 (first entry)

XX

DE SynBl transduction peptide.

XX

KW Pharmaceutical; nucleic acid delivery; transportan.

XX

OS Synthetic.

XX

PN US2005153913-A1.

XX

PD 14-JUL-2005.

XX

PF 28-JUN-2004; 2004US-00878175.

XX

PR 10-APR-2001; 2001US-00829551.

XX

PA (KOSA/) KOSAK K M.

XX

PI Kosak KM;

XX

XX WPI; 2005-496857/50.

XX

XX Pharmaceutical nucleic acid carrier composition useful in therapeutic

XX applications for targeting delivery of nucleic acids to their site of

XX action, having carrier substance covalently/non-covalently coupled to

XX nucleic acid intercalator.

XX

XX Disclosure; SEQ ID NO 36; 38pp; English.

XX

XX The invention relates to a pharmaceutical nucleic acid carrier

XX composition (C1), comprising a carrier substance covalently or non-

XX covalently coupled to a nucleic acid intercalator, where the nucleic acid

XX intercalator is coupled to a nucleic acid. C1 can be synthesized by

XX coupling a carrier substance to intercalator to produce a carrier

XX substance having intercalator coupled to it, and combining the

intercalator coupled carrier substance, with a nucleic acid, to allow intercalation of the coupled intercalator and the nucleic acid. (Cl) further comprising a targeting molecule or transduction vector coupled to the carrier substance. The covalent coupling of the carrier substance to intercalator is a bioleavable linkage chosen from a hydrazine linkage, disulfide linkage, protected disulfide linkage, ester linkage, ortho ester linkage, phosphonamide linkage, bioleavable polypeptide, aromatic azo linkage and aldehyde bond. (Cl) further comprising a chloroquine substance coupled to the carrier substance. The carrier substance is chosen from avidins, streptavidins, liposomes, micelles and dendrimers. The method further involves coupling targeting molecule or transduction vector to the carrier substance, or coupling chloroquine substance to the carrier. (Cl) is useful for delivering nucleic acids for therapeutic or other medicinal uses. (Cl) is useful for targeting the delivery of nucleic acids to their site of action. (Cl) delivers nucleic acids into site of action and improves their effectiveness. The present sequence represents a transduction peptide that can be used as the transduction vector in the method of the invention.

SQ Sequence 18 AA;

Query Match 100.0%; Score 91; DB 9; Length 18;  
Best Local Similarity 100.0%; Pred. No. 1.9e-07;  
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 RGGRLSYRRRFFSTGTGR 18  
|||||  
DB 1 RGGRLSYRRRFFSTGTGR 18

RESULT 21

ADE51567  
ID ADE51567 standard; peptide; 19 AA.

XX AC ADE51567;

DT 29-JAN-2004 (first entry)

DE Peptide #5 to transport cyclosporin compound across blood brain barrier.

XX neuroprotective; cerebroprotective; vulnery; hemostatic;  
XX anticonvulsant; neuroleptic; thrombolytic; anticoagulant; vasotropic;  
XX nootropic; antiparkinsonian; cytotatic; antidiabetic; antibacterial;  
XX anti-HIV; ophthalmological; antinflammatory; virucide; protozoacide;  
XX immunosuppressive; dermatological; antithyroid; antidote; antirheumatic;  
XX antiarthritic; antipsoriatic; endocrine-General; cyclophilin inhibitor;  
XX calcineurin inhibitor;  
XX neurotoxic calcium-dependent enzyme cascade blocker;  
XX mitochondrial stabilizer; cyclosporin; transporter; blood-brain barrier.

XX Synthetic.

XX W02003070755-A2.

XX PD 28-AUG-2003.

XX PF 24-FEB-2003; 2003WO-FR000591.

XX PR 22-FEB-2002; 2002FR-00002299.

XX PA (SYNT-) SYNT-EM.

XX PA (MAAS-) MAAS BIOLAB LLC.

XX P1 Mouchet P, Rees AR, Elmer E, Keep MF;

XX WP1; 2003-712609/67.

XX New cyclosporin derivatives, containing bonded peptide vector for crossing blood-brain barrier, used for treating cerebral disorders such as neurodegenerative diseases, cerebral trauma or cerebrovascular accidents.

PS Disclosure; SEQ ID NO 5; 77pp; French.

XX

The invention relates novel cyclosporin compounds (I) comprise at least one cyclosporin molecule (II) and at least one peptide vector (III) capable of transporting (I) across the blood-brain barrier. (I) are used for the treatment or prevention of: (i) acute neurological disorders, e.g. due to traumatic cerebral lesions, spinal cord lesions, exposure to radiation, chemotherapy, epilepsy, schizophrenia, cerebral or spinal surgery, cerebrovascular accidents, embolic cerebrovascular accident, global cerebral ischemia, ruptured aneurysms, subarachnoid hemorrhage, vascular spasms or hemorrhagic vascular accidents; (ii) neurodegenerative diseases selected from Alzheimer's disease, Parkinson's disease, Huntington's disease, Down syndrome, Charcot disease, spino-muscular atrophy, bulbar paralysis, schizophrenia, Tourette syndrome, diffuse cerebrocortical atrophy, Lewy body dementia, mesolimbocortical dementia, thalamic degeneration, Pick disease, multisystem dementia, cortico-striato-spinal degeneration, Shy-Drager syndrome, Richardson-Steels-Olzewski syndrome, Parkinson-amyotrophic lateral sclerosis-Guam dementia complex, post-polio syndrome, olivo-cerebellar atrophy, Friedreich ataxia, paraneoplastic syndrome, traumatic chronic encephalopathy (boxer's dementia), Wilson disease, Menke disease, Tay-Sachs gangliosidosis, Krabbe disease, peripheral neuropathy, diabetic neuropathy or aging; (iii) prion diseases, such as Creutzfeldt Jacob disease (CJD), atypic CJD, kuru, scrapie or bovine spongiform encephalitis; (iv) retroviral diseases, e.g. AIDS dementia, AIDS myelopathy, AIDS peripheral neuropathy or tropical paraparesis; (v) visual and retinal disorders, e.g. glaucoma-related degeneration, macular degeneration, diabetic degeneration, diabetic retinopathy, degeneration-related inflammation, detached retina, optical neuritis, optic nerve lesions, optical chiasm or optical tractus and retinal lesions caused by photons, trauma, ischemia or elevated intracranial pressure; (vi) viral and bacterial diseases associated with encephalopathy, including herpetic, equine, post-vaccination, Japanese or Nile encephalitis, meningitis, rabies, poliomyelitis, progressive multifocal leuko-encephalopathy, subacute sclerotic panencephalitis, cerebral malaria, Lyme disease or neurosyphilis; (vii) immunological diseases, e.g. plaque sclerosis, Guillain-Barre syndrome, lupus erythematosus or Graves disease; (viii) the effects of neurotoxins, including aminoglycosides, chlorinated hydrocarbons, organophosphates, insecticides, herbicides, paraquat, nerve gas, 1-methyl-4-phenyl-1,2,3,6-tetrahydropyridine, rotenone, cyanide, carbon monoxide, methanol, ethanol, mercury, arsenic, chemotherapeutic agents (e.g. methotrexate, mercaptopurine, fluorouracil, nitrosoureas, hydroxyurea, cisplatin, carboplatin, daunorubicin, etoposide, vincristine, vinblastine, taxol (or derivatives) or cyclophosphamide) or corticosteroids; (ix) metabolic encephalopathy, e.g. hepatic or uremic encephalopathy; (x) conditions requiring induction of a non-immune state, e.g. transplantation of organs, tissues or cells or immune or autoimmune diseases such as rheumatoid arthritis, eczema, psoriasis or alopecia; or (xi)) chemotherapy-resistant tumors. This sequence is an example of the peptide part of the compound.

SQ Sequence 19 AA;

Query Match 100.0%; Score 91; DB 7; Length 19;  
Best Local Similarity 100.0%; Pred. No. 1.9e-07;  
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 RGGRLSYRRRFFSTGTGR 18  
|||||  
DB 2 RGGRLSYRRRFFSTGTGR 19

RESULT 22

ADR88700  
ID ADR88700 standard; peptide; 19 AA.

XX AC ADR88700;

XX

DT 18-NOV-2004 (first entry)

DE Amino acid sequence of a peptide designated Gly-SynB1.

XX disease treatment; active substance transport; bioavailability;  
KW Gly-SynB1; cyclosporin A.

XX OS Unidentified.  
XX PN FR2851471-A1.  
XX PD 27-AUG-2004.  
XX PF 24-FEB-2003; 2003FR-00002242.  
XX PR 24-FEB-2003; 2003FR-00002242.  
XX PA (SYNT-) SYNT:EM SA.  
XX PI Rees AR, Mouchet P;  
XX DR WPI; 2004-627939/61.  
XX CC Compound comprising active agent coupled to vector through a linker,  
PT useful in human or veterinary medicine, where the linker includes a  
PT hydroxyproline residue.  
XX PS Disclosure; SEQ ID NO 5; 65pp; French.  
XX CC The specification describes a compound comprising at least one active  
CC substance and at least one vector, connected by a linker that includes a  
CC hydroxyproline residue. The linker is of a formula given in the  
CC specification. The vector modifies the physicochemical or pharmacokinetic  
CC properties of the active substance. The active substance is a protein,  
CC (poly)peptide, antibody (or fragment), nucleic acid, oligonucleotide,  
CC ribozyme, or a chemical for treatment or prevention of human or animal  
CC disease, e.g. an antitumour or antiviral agent. Alternatively, it is a  
CC radioactive or coloured material, or some other substance suitable as  
CC indicator of metabolism or disease. Compounds of the invention are used  
CC for treatment, prevention and diagnosis of disease in human or veterinary  
CC medicine. They facilitate transport of the active substance across  
CC biological barriers and its penetration into cells, and they also modify  
CC the bioavailability or solubility of active substances. The present  
CC sequence represents a peptide designated Gly-Synbl. Gly-Synbl was joined  
CC to cyclosporin A via a linker to produce exemplary compounds of the  
XX invention.  
XX SQ Sequence 19 AA;  
Query Match 100.0%; Score 91; DB 8; Length 19;  
Best Local Similarity 100.0%; Pred. No. 1.9e-07;  
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
QY 1 RGGRLSYRRRRFSTSTGR 18  
DB 2 RGGRLSYRRRRFSTSTGR 19  
RESULT 23  
AAW99403  
ID AAW99403 standard; peptide; 18 AA.  
AC AAW99403;  
XX 08-JUN-1999 (first entry)  
XX Protegrin derivative peptide SMI738.  
XX Linear; protegrin; peptide antibiotic; beta-sheet; secondary structure;  
KW disulphide bridge; antibody; ribozyme; antitumour agent; antiviral;  
KW anti-inflammatory; mammal; cell membrane; passive transport; cytoplasm;  
KW nucleus; blood-brain barrier.  
XX Synthetic.  
OS WO9907728-A2.  
XX 18-FEB-1999.

PF 06-AUG-1998; 98WO-FR001757.  
XX 12-AUG-1997; 97FR-00010297.  
XX (SYNT-) SYNT:EM SA.  
XX Calas B, Grassy G, Chavanieu A, Kaczorek M;  
PI WPI; 1999-190034/16.  
XX Derivatives of antibiotic peptides lacking disulfide bridges - used as  
PT carriers to deliver active agents into cells.  
XX Claim 7; Page 28; 37pp; French.  
XX This peptide represents a linear derivative of the protegrin family of  
CC peptide antibiotics. Protegrin antibiotics form part of the peptide  
CC antibiotic family which contain a beta-sheet secondary structure linked  
CC by disulphide bridges. The new derivatives are linear and lack the  
CC disulphide bridge. The novel derivatives are used to deliver active  
CC agents to an organism, e.g. therapeutic proteins, antibodies (or their  
CC fragments), nucleic acid, oligonucleotides, ribozymes, antitumour agents,  
CC antivirals and anti-inflammatories, etc. The derivatives are non-toxic  
CC and non-lytic but can cross mammalian cell membranes rapidly by a passive  
CC mechanism, so can deliver active agents to cytoplasm and nucleus,  
CC including crossing the blood-brain barrier  
XX SQ Sequence 18 AA;  
Query Match 89.0%; Score 81; DB 2; Length 18;  
Best Local Similarity 88.9%; Pred. No. 7.5e-06;  
Matches 16; Conservative 0; Mismatches 2; Indels 0; Gaps 0;  
QY 1 RGGRLSYRRRRFSTSTGR 18  
DB 1 RGGRLSYRRRRFSTSTGR 18  
RESULT 24  
AAW93616  
ID AAW93616 standard; peptide; 18 AA.  
XX AAW93616;  
XX 25-SEP-2000 (first entry)  
XX Peptide which may be linked to anticancer agents.  
XX Anticancer agent; cancer cell; resistance; P-glycoprotein pump; cancer.  
XX Unidentified.  
XX WO200032237-A1.  
XX 08-JUN-2000.  
XX 26-NOV-1999; 99WO-FR002939.  
XX 30-NOV-1998; 98FR-00015073.  
XX (SYNT-) SYNT:EM SA.  
XX Tamsamani J, Kaczorek M, Colin De Verdiere A;  
XX WPI; 2000-412166/35.  
XX New composition useful for cancer treatment and prevention, contains  
PT anticancer agent and peptide vector that transports agent into cells.  
XX Disclosure; Page 8; 34pp; French.  
XX The specification describes a pharmaceutical composition, which comprises  
CC at least one anticancer agent associated with at least one peptide that



CC can transport it into cancer cells and which inhibits development of  
 CC resistance to the anticancer agent. By using the peptide as a vector for  
 CC delivery of the anticancer agent, mechanisms that cause cancer cells to  
 CC become resistant to the agent, particularly the P-glycoprotein pump, are  
 CC avoided. Also, peptides are easily produced by chemical synthesis, can be  
 CC coupled easily to the agent, cross mammalian cell membranes rapidly by a  
 CC passive mechanism (no receptors required), and are non-toxic and non-  
 CC lytic. The compositions are used to treat cancer. The present sequence  
 CC represents a peptide which may be linked to the anticancer agents of the  
 CC invention  
 XX  
 CC  
 SQ Sequence 18 AA;

Query Match 89.0%; Score 81; DB 3; Length 18;  
 Best Local Similarity 88.9%; Pred. No. 7.5e-06;  
 Matches 16; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1 RGGRLSYRRRPFSTGTGR 18  
 |||||  
 DB 1 RGGRLSYRRRPFVSVGR 18

## RESULT 25

ABR43977  
 ID ABR43977 standard; peptide; 18 AA.

AC ABR43977;

DT 11-AUG-2003 (first entry)

DE Beta-stranded antibiotic peptide linear derivative.

XX Antibiotic; antigen; immunostimulant; vaccine; immune response.

XX Synthetic.

XX WO2003033021-A1.

XX 24-APR-2003.

XX 15-OCT-2002; 2002WO-EP011500.

XX 16-OCT-2001; 2001EP-00402671.

XX (SYNT-) SYNT:EM SA.

XX Johnson ME, Hamilton Day F, Kaczorek M, Tamsamani J;

XX WPI; 2003-430304/40.

XX New conjugates of antigens, which are coupled to a linear derivative of a  
 PT beta-stranded antibiotic peptide, useful for enhancing the immune  
 PT response of a mammal to an antigen, particularly useful in vaccination or  
 PT prophylaxis.

XX Claim 7; Page 27; 57pp; English.

XX The invention relates to a conjugate of an antigen, which is coupled to a  
 CC linear derivative of a beta-stranded antibiotic peptide. The conjugate is  
 CC useful for enhancing the immune response of a mammal to an antigen. The  
 CC conjugate is particularly useful in vaccination or prophylaxis. The  
 CC present sequence represents a linear derivative of a beta-stranded  
 CC antibiotic peptide  
 XX  
 CC

SQ Sequence 18 AA;

Query Match 89.0%; Score 81; DB 6; Length 18;  
 Best Local Similarity 88.9%; Pred. No. 7.5e-06;  
 Matches 16; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1 RGGRLSYRRRPFSTGTGR 18  
 |||||  
 DB 1 RGGRLSYRRRPFVSVGR 18

RESULT 26  
 ADN03481  
 ID ADN03481 standard; peptide; 18 AA.  
 XX  
 AC ADN03481;  
 XX  
 DT 01-JUL-2004 (first entry)  
 XX  
 DE Beta-stranded proteogrin peptide linear deriative #4.

XX Beta-stranded antibiotic peptide; immune response; therapy; vaccine;  
 KW proteogrin.

XX Unidentified.

XX US2004072340-A1.

XX 15-APR-2004.

XX 15-OCT-2002; 2002US-00270010.

XX 15-OCT-2002; 2002US-00270010.

XX (JOHN/) JOHNSON M E.

XX (DAYF/) HAMILTON DAY F.

XX (KACZ/) KACZOREK M.

XX (TEMS/) TEMSAMANI J.

XX Johnson ME, Hamilton Day F, Kaczorek M, Tamsamani J;

XX WPI; 2004-328576/30.

XX New conjugates of an antigen coupled to a linear derivative of a beta-  
 PT stranded antibiotic peptide, useful for enhancing the immune response of  
 PT a mammal to an antigen.

XX Claim 7; SEQ ID NO 7; 21pp; English.

XX The present invention relates to conjugates of an antigen coupled to a  
 CC linear derivative of a beta-stranded antibiotic peptide. The invention is  
 CC useful for enhancing the immune response of a mammal to an antigen. The  
 CC invention is also useful in the production of vaccines. The present  
 CC sequence is a beta-stranded proteogrin (antibiotic) peptide linear  
 CC derivative.  
 XX  
 CC

SQ Sequence 18 AA;

Query Match 89.0%; Score 81; DB 8; Length 18;  
 Best Local Similarity 88.9%; Pred. No. 7.5e-06;  
 Matches 16; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1 RGGRLSYRRRPFSTGTGR 18  
 |||||  
 DB 1 RGGRLSYRRRPFVSVGR 18

## RESULT 27

AAE29879

ID AAE29879 standard; peptide; 18 AA.

XX AAE29879;

XX 24-FEB-2003 (first entry)

XX Membrane translocation peptide, penetratin.

XX Gonadotrophin releasing hormone analogue; neurotoxin; prostate cancer;  
 KW endocrine disorder; gonadotrophin related illness; endometrial cancer;  
 KW pancreatic cancer; breast cancer; endometriosis; precocious puberty;  
 KW GnRH-A; therapy; penetratin.  
 XX



Matches 15; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Qy 1 RGGRLSYRRRPFSTGCR 18  
 ||||| |||||  
 Db 1 RGGRLSYXXXFFSTGCR 18

RESULT 30  
 ADH59545  
 ID ADH59545 standard; peptide; 18 AA.  
 AC ADH59545;  
 XX  
 DT 25-MAR-2004 (first entry)  
 XX  
 DB SynB6 peptide.  
 XX  
 KW lung cancer; pulmonary disease; SynB4; SynB6; Cytostatic; Antibiotic;  
 KW Antibacterial; Tuberculostatic; Antiinflammatory.  
 XX  
 OS Unidentified.  
 XX  
 PN WO2003105907-A2.  
 XX  
 PD 24-DEC-2003.  
 XX  
 PF 18-JUN-2003; 2003WO-FR001864.  
 XX  
 PR 18-JUN-2002; 2002FR-00007493.  
 XX  
 PA (SYNT-) SYNT:EM.  
 XX  
 PI Tamsamani J, Rees AR, Rouselle C;  
 XX  
 DR WPI; 2004-090759/09.  
 XX  
 PT New compounds useful for treating e.g. lung cancer or pulmonary diseases,  
 PT comprises active agent e.g. doxorubicin, bonded to peptide carrier to  
 PT increase bioavailability in lungs.  
 XX  
 PS Claim 1; SEQ. ID NO 2; 19pp; French.  
 XX  
 CC The present invention relates to new compounds comprising at least one  
 CC therapeutic agent for the treatment of lung cancer or pulmonary diseases  
 CC and at least one carrier peptide for increasing the bioavailability of  
 CC the compounds in the lungs, being one of two specific peptides designated  
 CC SynB4 and SynB6. The compounds are used for treating lung cancer or  
 CC pulmonary diseases. The pulmonary diseases include bronchitis, emphysema,  
 CC pneumonia (e.g. pneumonia caused by opportunistic *Pseudomonas* bacteria),  
 CC cystic fibrosis and tuberculosis ( *Mycobacterium tuberculosis* infection).  
 CC The peptide transports the active agent selectively to the lungs, thus  
 CC increasing the bioavailability of the compound and promoting  
 CC incorporation of the compound into the lungs and reducing side-effect  
 CC problems. The present sequence represents SynB6 peptide.  
 XX  
 SQ Sequence 18 AA;  
 XX  
 Query Match 80.2%; Score 73; DB 8; Length 18;  
 Best Local Similarity 83.3%; Pred. No. 0.00015;  
 Matches 15; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Qy 1 RGGRLSYRRRPFSTGCR 18  
 ||||| |||||  
 Db 1 RGGRLSYXXXFFSTGCR 18

RESULT 31  
 AAM48475  
 ID AAM48475 standard; peptide; 18 AA.  
 AC AAM48475;  
 XX  
 DT 28-MAY-2002 (first entry)

XX Antibiotic peptide PG-4A.  
 DB  
 XX Amphipathic peptide; antibiotic peptide; carrier.  
 KW  
 XX  
 OS Synthetic.  
 XX  
 PN WO200202595-A1.  
 XX  
 PD 10-JAN-2002.  
 XX  
 PF 03-JUL-2001; 2001WO-FR002129.  
 XX  
 PR 03-JUL-2000; 2000FR-00008633.  
 XX  
 PA (SYNT-) SYNT:EM SA.  
 XX  
 PI Drin G, Gomar J, Tamsamani J, Rees AR;  
 XX  
 DR WPI; 2002-241369/29.  
 XX  
 PT New amphipathic derivatives of antibiotic peptides, are useful for  
 PT delivering therapeutic and diagnostic agents to cells, provides efficient  
 PT transport across membranes.  
 XX  
 PS Claim 8; Page 24; 49pp; French.  
 XX  
 CC The present invention related to novel amphipathic antibiotic peptides.  
 CC The present sequence is one such peptide. The peptides are useful as  
 CC carriers for delivering attached active agents to cells, specifically to  
 CC a target site in cytoplasm or the nucleus, for therapeutic or diagnostic  
 CC use  
 XX  
 SQ Sequence 18 AA;  
 XX  
 Query Match 75.8%; Score 69; DB 5; Length 18;  
 Best Local Similarity 66.7%; Pred. No. 0.00064;  
 Matches 12; Conservative 4; Mismatches 2; Indels 0; Gaps 0;

Qy 1 RGGRLSYRRRPFSTGCR 18  
 ||||| |||||  
 Db 1 RGGRLAYRRRFAVAVGR 18

RESULT 32  
 AAW18153  
 ID AAW18153 standard; peptide; 18 AA.  
 XX  
 AC AAW18153;  
 XX  
 DT 25-MAR-2003 (revised)  
 DT 11-AUG-1997 (first entry)  
 XX  
 DE Cationic, antimicrobial, virus-neutralising protegrin PC-57.  
 XX  
 KW Antibacterial; antiviral; antifungal; antibiotic; endotoxin;  
 KW Candida albicans; gram-negative bacteria; STD;  
 KW sexually transmitted disease; HIV-1; Chlamydia trachomatis;  
 KW Treponema pallidum; Neisseria gonorrhoeae; eye care; preservative; food.  
 XX  
 OS Synthetic.  
 XX  
 PN WO9637508-A1.  
 XX  
 PD 28-NOV-1996.  
 XX  
 PF 24-MAY-1996; 96WO-US0007594.  
 XX  
 PR 26-MAY-1995; 95US-00451832.  
 PR 07-JUL-1995; 95US-00499523.  
 XX  
 PA (REGC ) UNIV CALIFORNIA.  
 XX

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PI  Lehrer RI, Kokryakov VN, Harwig SS;
XX  WPI; 1997-033984/03.
XX
XX  Cationic, antimicrobial, virus-neutralising protegrin peptide(s) - useful
PT  for the treatment of microbial infection, as food preservatives and in
PT  eye care solutions.
XX
XX  Claim 6; Page 64; 106pp; English.
XX
XX  The present sequence is a specifically claimed example of a peptide,
CC  recombinantly produced, corresponding to the generic formula: A1-A2-A3-A4
CC  -A5-Cys-A7-Cys-A9-A10-A11-A12-Cys-A14-Cys-A16-(A17-A18) where A1 = a
CC  basic amino acid; A2 and A3 = a small amino acid; A4 = a basic or small
CC  amino acid; A5, A7 and A14 = a hydrophobic amino acid; A9, A12 and A16 = a
CC  basic, hydrophobic, neutral/polar or small amino acid; A10 and A11 = a
CC  basic, hydrophobic, neutral/polar or small amino acid or proline; A17 may
CC  be absent or a basic, neutral/polar, hydrophobic or small amino acid; and
CC  A18 may be absent or a basic, neutral/polar, hydrophobic or small amino
CC  acid. This has a charge of at least +3 and its N-terminal acylated and/or
CC  C-terminal amidated or esterified forms, all of which may contain a
CC  disulphide bond to give a cysteine bridge. This peptide is in snake form
CC  where all the cystine residues are replaced by a hydrophobic, small or
CC  large polar amino acid (e.g. alanine in this case). Peptides of this
CC  formula are designated protegrins and are useful as anti-bacterial, anti-
CC  viral and anti-fungal agents in plants and animals. The protegrins confer
CC  resistance to microbial or viral infection in plants by preventing the
CC  growth of a virus or microbe and inactivate the endotoxin of gram-
CC  negative bacteria. The protegrins are particularly useful for the
CC  treatment of sexually transmitted disease caused by microorganisms e.g.
CC  Candida albicans, HIV-1, Chlamydia trachomatis, Treponema pallidum and
CC  Neisseria gonorrhoeae. They can also be used in eye care solutions and as
CC  preservatives for food. The protegrins are more effective under
CC  physiological conditions (e.g. in the presence of serum) than certain
CC  antibiotics and are non-toxic to the cells of higher organisms. (Updated
XX  on 25-MAR-2003 to correct PA field.)
XX
XX  Sequence 18 AA;
XX
XX  Query Match 73.6%; Score 67; DB 2; Length 18;
XX  Best Local Similarity 66.7%; Pred. No. 0.0013;
XX  Matches 12; Conservative 4; Mismatches 2; Indels 0; Gaps 0;

QY  1 RGGRLSYSRRRFSTGTGR 18
DB  |||||:||||: ||
    1 RGGRLAYARRRFAVWGR 18

RESULT 33
ADL18453
XX  ADL18453 standard; peptide; 18 AA.
XX
XX  ADL18453;
XX  AC
XX  XX
XX  06-MAY-2004 (first entry)
XX
XX  Antimicrobial protegrin peptide PC-57.
XX
XX  virucide; antimicrobial; peptide therapy; recombinant peptide compound;
XX  antiviral; viral infection; microbial infection; endotoxin inactivation;
KW  eye care; contact lens solution; topical composition;
KW  pharmaceutical composition; sexually transmitted disease; STD; protegrin.
XX
XX  Synthetic.
XX
XX  Key Location/Qualifiers
XX  Modified-site 18
XX  FT /label= OTHER
XX  FT /note= "OTHER= C-terminal amidation"
XX
XX  US6653442-B1.
XX  PN
XX  25-NOV-2003.
XX  PD

Lehrer RI, Chen J, Steinberg DA, Lehrer RI, Harwig SS;
Kokryakov VN;
WPI; 2004-068297/07.
New peptide in its N-terminal acylated or C-terminal amidated or
esterified form in linear or cysteine-bridged form, useful for treating
sexually transmitted diseases and as preservatives.
Claim 1; SEQ ID NO 93; 84pp; English.
The invention describes a purified and isolated or recombinantly produced
peptide compound selected from any of the 43 fully defined sequences of
16-18 amino acids, given in the specification, or its N-terminal acylated
or C-terminal amidated or esterified forms in linear or cysteine-bridged
form. Also described are: a pharmaceutical composition for antimicrobial
or antiviral use, comprising any of the peptides cited above in admixture
with at least one excipient; and a composition for application to plants
or plant environments for conferring resistance to microbial or viral
infections in plants comprising any of the peptides cited above in
admixture with at least one diluent. The peptides are useful as
preservatives and in preventing, treating or ameliorating viral or
microbial infections in animals and plants, and in inactivating
endotoxins. They are particularly useful in eye care, such as in contact
lens solutions, and in topical and pharmaceutical compositions for
treating sexually transmitted diseases (STDs). This is the amino acid
sequence of an antimicrobial protegrin peptide of the invention.
Sequence 18 AA;
Query Match 73.6%; Score 67; DB 8; Length 18;
Best Local Similarity 66.7%; Pred. No. 0.0013;
Matches 12; Conservative 4; Mismatches 2; Indels 0; Gaps 0;

QY  1 RGGRLSYSRRRFSTGTGR 18
DB  |||||:||||: ||
    1 RGGRLAYARRRFAVWGR 18

RESULT 34
AAY22007
XX  AAY22007 standard; peptide; 18 AA.
XX
XX  AC
XX  AAY22007;
XX
XX  23-AUG-1999 (first entry)
XX
XX  Antimicrobial peptide derivative of protegrin.
XX
XX  Antimicrobial peptide; protegrin; microbe growth inhibitor; Pseudomonas;
KW  microbial infection; Staphylococcus aureus; Helicobacter pylori; therapy;
KW  antibiotic-resistant bacterium; disinfectant composition; preservative;
KW  haemolytic activity; systemic antibiotic.
XX
XX  Sus scrofa.
XX
XX  WO9927945-A1.
XX  PN
XX  10-JUN-1999.
XX  PD
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XX PF 01-DEC-1998; 98WO-US025458.
XX XX
XX PR 03-DEC-1997; 97US-00984294.
XX XX
XX PA (INTR-) INTRABIOTICS PHARM INC.
XX XX
XX PI Chang CC, Chen J, Lehrer RI, Radel PA;
XX DR WPI; 1999-385321/32.
XX XX
XX PT Antimicrobial threonine-containing protegrins.
XX XX
XX PS Claim 11; Page 52; 75pp; English.
XX XX
XX CC This sequence represents an example of an antimicrobial peptide (I) of
CC the invention, and comprises 10-30 amino acid residues based on a
CC naturally-occurring protegrin peptide. The antimicrobial peptide is
CC useful in environmental composition for application to plants or plant
CC environments, for inhibiting the growth of microbes. The peptide is
CC useful for treating or preventing microbial infections, e.g. caused by
CC Staphylococcus aureus, Pseudomonas, Helicobacter pylori or an antibiotic-
CC resistant bacterium, or related diseases. The peptide can be used to
CC inactivate the endotoxin of Gram-negative bacteria. The peptides can be
CC used in disinfectant compositions, and as preservatives for materials
CC such as foodstuffs, cosmetics, medicaments or other materials containing
CC nutrients for organisms. The peptides exhibit decreased haemolytic
CC activity against human red blood cells as compared with native PG-1 and
CC melittin. They have improved serum compatibility and therefore improved
CC use as systemic antibiotics. At the same time the peptides provide broad
CC spectrum activity with a low frequency of resistance
XX SQ Sequence 18 AA;
XX
XX Query Match 72.5%; Score 66; DB 2; Length 18;
XX Best Local Similarity 72.2%; Pred. No. 0.002;
XX Matches 13; Conservative 0; Mismatches 5; Indels 0; Gaps 0;
XX
XX QY 1 RGGRLSYRRRPFSTGCR 18
XX ||||| ||||| |||
XX DB 1 RGGRLCYCRRRPFCTGCR 18
XX
XX RESULT 36
XX AAW36429
XX ID AAW36429 standard; peptide; 18 AA.
XX XX
XX AC AAW36429;
XX XX
XX DT 13-FEB-1998 (first entry)
XX XX
XX DE Antimicrobial protegrin peptide (229).
XX XX
XX KW Antimicrobial protegrin; broad spectrum; gram-positive; bacterium;
XX KW gram-negative; bacteria; yeast; fungus; protozoa; virus;
XX KW retrovirus; HIV; human immunodeficiency virus; preservation;
XX KW disinfection; prophylaxis; treatment; infection; disease; conjunctivitis;
XX KW keratitis; corneal ulcer; stomach ulcer; STD; Helicobacter pylori;
XX KW sexually transmitted disease; oral mucositis; gram-negative sepsis;
XX KW endocarditis; pneumonia; biocidal; biostatic; respiratory infection;
XX KW urinary tract infection; MRSA; protozoan;
XX KW vancomycin resistant Enterococcus; pathogen; multi-drug resistance;
XX KW penicillin resistant Streptococcus pneumoniae; pig; porcine;
XX KW methicillin resistant Staphylococcus aureus; systemic candidiasis.
XX XX
XX OS Synthetic.
XX OS Sus scrofa.
XX XX
XX PN WO9718826-A1.
XX XX
XX PD 29-MAY-1997.
XX XX
XX PF 22-NOV-1996; 96WO-US018544.
XX XX
XX PR 22-NOV-1995; 95US-00562346.
XX PR 17-MAY-1996; 96US-00649811.
XX PR 01-AUG-1996; 96US-00690921.
XX PR 21-NOV-1996; 96US-00752852.
XX XX
XX PA (INTR-) INTRABIOTICS PHARM INC.
XX PA (REGC) UNIV CALIFORNIA.
XX XX
XX PI Chang CC, Gu CL, Chen J, Steinberg DA, Lehrer RI;
XX DR WPI; 1999-385321/32.

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XX DR WPI; 1997-297871/27.
XX PT New antimicrobial protegrin peptide(s) - having activity against
XX PT bacteria, yeast, fungi, protozoa and certain strains of viruses (e.g.
XX PT HIV).
XX PS Claim 23; Page 110; 130pp; English.
XX CC The present sequence is an antimicrobial protegrin peptide, which has a
XX CC broad spectrum of activity against microbial targets, including gram-
XX CC positive and gram-negative bacteria, yeast, fungi, protozoa and certain
XX CC strains of viruses and retroviruses, e.g. HIV. It can be used to preserve
XX CC or disinfect a variety of materials, including medical equipment.
XX CC foodstuffs, cosmetics, contact lens solutions, medicaments or other
XX CC nutrient containing materials. It can also be used for the prophylaxis or
XX CC treatment of microbial infections or diseases in plants and animals, e.g.
XX CC conjunctivitis, keratitis, corneal ulcers, stomach ulcers associated with
XX CC Helicobacter pylori, sexually transmitted diseases, gram-negative sepsis,
XX CC endocarditis, pneumonia and other respiratory infections, urinary tract
XX CC infections, systemic candidiasis and oral mucositis. It is biostatic or
XX CC biocidal against clinically relevant pathogens exhibiting multi-drug
XX CC resistance, e.g. vancomycin resistant Enterococcus faecium or faecalis,
XX CC penicillin resistant Streptococcus pneumoniae and methicillin resistant
XX CC Staphylococcus aureus (MRSA). It is given at a dosage of 0.1 to 5,
XX CC preferably 0.5 to 1 mg/kg/day, by injection
XX SQ Sequence 18 AA;

Query Match 71.4%; Score 65; DB 2; Length 18;
Best Local Similarity 66.7%; Pred. No. 0.0028;
Matches 12; Conservative 2; Mismatches 4; Indels 0; Gaps 0;

QY 1 RGRRLSYRRRPFSTGTGR 18
Db 1 RGRRLCYARRRFAVCVGR 18

RESULT 37
AAW09085
ID AAW09085 standard; peptide; 18 AA.
AC AAW09085;
DT 25-MAR-2003 (revised)
DT 11-AUG-1997 (first entry)
XX Cationic, antimicrobial, virus-neutralising protegrin IB-289.
XX Antibacterial; antiviral; antifungal; antibiotic; endotoxin;
XX Candida albicans; gram-negative bacteria; STD;
XX sexually transmitted disease; HIV-1; Chlamydia trachomatis;
XX Treponema pallidum; Neisseria gonorrhoeae; eye care; preservative; food.
XX Synthetic.
XX Key Location/Qualifiers
FH Modified-site 1 /note= "Acylated"
FT Disulfide-bond 6..15 /note= "results in bullet form peptide"
FT Modified-site 18 /note= "Amidated"
XX WO9637508-A1.
XX 28-NOV-1996.
XX 24-MAY-1996; 96WO-US0007594.
XX 26-MAY-1995; 95US-00451832.
XX 07-JUL-1995; 95US-00499523.
XX

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PA (REGC ) UNIV CALIFORNIA.
PI Lehrer RI, Kokryakov VN, Harwig SS;
XX WPI; 1997-033984/03.
XX Cationic, antimicrobial, virus-neutralising protegrin peptide(s) - useful
XX PT for the treatment of microbial infection, as food preservatives and in
XX PT eye care solutions.
XX Claim 6; Page 65; 106pp; English.
XX The present sequence is a specifically claimed example of a peptide,
XX CC recombinantly produced, corresponding to the generic formula: A1-A2-A3-A4
XX CC -A5-Cys-A7-Cys-A9-A10-A11-A12-Cys-A14-Cys-A16-(A17-A18) where A1 = a
XX CC basic amino acid; A2 and A3 = a small amino acid; A4 = a basic or small
XX CC amino acid; A5, A7 and A14 = a hydrophobic amino acid; A9, A12 and A16 =
XX CC a basic, hydrophobic, neutral/polar or small amino acid; A10 and A11 = a
XX CC basic, hydrophobic, neutral/polar or small amino acid or proline; A17 may
XX CC be absent or a basic, neutral/polar, hydrophobic or small amino acid; and
XX CC A18 may be absent or a basic, neutral/polar, hydrophobic or small amino
XX CC acid. This has a charge of at least +3 and its N-terminal acylated and/or
XX CC C-terminal amidated or esterified forms, all of which may contain a
XX CC disulphide bond to give a cysteine bridge. Peptides of this formula are
XX CC designated protegrins and are useful as anti-bacterial, anti-viral and
XX CC anti-fungal agents in plants and animals. The protegrins confer
XX CC resistance to microbial or viral infection in plants by preventing the
XX CC growth of a virus or microbe and inactivate the endotoxin of gram-
XX CC negative bacteria. The protegrins are particularly useful for the
XX CC treatment of sexually transmitted disease caused by microorganisms e.g.
XX CC Candida albicans, HIV-1, Chlamydia trachomatis, Treponema pallidum and
XX CC Neisseria gonorrhoeae. They can also be used in eye care solutions and as
XX CC preservatives for food. The protegrins are more effective under
XX CC physiological conditions (e.g. in the presence of serum) than certain
XX CC antibiotics and are non-toxic to the cells of higher organisms. (Updated
XX CC on 25-MAR-2003 to correct PA field.)
XX SQ Sequence 18 AA;

Query Match 71.4%; Score 65; DB 2; Length 18;
Best Local Similarity 66.7%; Pred. No. 0.0028;
Matches 12; Conservative 2; Mismatches 4; Indels 0; Gaps 0;

QY 1 RGRRLSYRRRPFSTGTGR 18
Db 1 RGRRLCYARRRFAVCVGR 18

RESULT 38
AAW09084
ID AAW09084 standard; peptide; 18 AA.
XX AAW09084;
XX 25-MAR-2003 (revised)
DT 11-AUG-1997 (first entry)
XX Cationic, antimicrobial, virus-neutralising protegrin IB-288.
XX Antibacterial; antiviral; antifungal; antibiotic; endotoxin;
XX Candida albicans; gram-negative bacteria; STD;
XX sexually transmitted disease; HIV-1; Chlamydia trachomatis;
XX Treponema pallidum; Neisseria gonorrhoeae; eye care; preservative; food.
XX Synthetic.
XX Key Location/Qualifiers
FH Modified-site 1 /note= "Acylated"
FT Disulfide-bond 6..15 /note= "results in bullet form peptide"
XX WO9637508-A1.

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XX PD 28-NOV-1996.  
 XX PF 24-MAY-1996; 96WO-US007594.  
 XX PR 26-MAY-1995; 95US-00451832.  
 XX PR 07-JUL-1995; 95US-00499523.  
 XX PA (REGC ) UNIV CALIFORNIA.  
 XX PI Lehrer RI, Kokryakov VN, Harwig SS;  
 XX DR WPI; 1997-033984/03.  
 XX PT Cationic, antimicrobial, virus-neutralising protegrin peptide(s) - useful  
 PT for the treatment of microbial infection, as food preservatives and in  
 PT eye care solutions.  
 XX PS Claim 6; Page 65; 106pp; English.  
 XX CC The present sequence is a specifically claimed example of a peptide,  
 CC recombinantly produced, corresponding to the generic formula: A1-A2-A3-A4  
 CC -A5-Cys-A7-Cys-A9-A10-A11-A12-Cys-A14-Cys-A16-(A17-A18) where A1 = a  
 CC basic amino acid; A2 and A3 = a small amino acid; A4 = a basic or small  
 CC amino acid; A5, A7 and A14 = a hydrophobic amino acid; A9, A12 and A16 =  
 CC basic, hydrophobic, neutral/polar or small amino acid; A10 and A11 = a  
 CC basic, hydrophobic, neutral/polar or small amino acid or proline; A17 may  
 CC be absent or a basic, neutral/polar, hydrophobic or small amino acid; and  
 CC A18 may be absent or a basic, neutral/polar, hydrophobic or small amino  
 CC acid. This has a charge of at least +3 and its N-terminal acylated and/or  
 CC C-terminal amidated or esterified forms, all of which may contain a  
 CC disulphide bond to give a cysteine bridge. Peptides of this formula are  
 CC designated protegrins and are useful as anti-bacterial, anti-viral and  
 CC anti-fungal agents in plants and animals. The protegrins confer  
 CC resistance to microbial or viral infection in plants by preventing the  
 CC growth of a virus or microbe and inactivate in plants by preventing the  
 CC negative bacteria. The protegrins are particularly useful for the  
 CC treatment of sexually transmitted disease caused by microorganisms e.g.  
 CC Candida albicans, HIV-1, Chlamydia trachomatis, Treponema pallidum and  
 CC Neisseria gonorrhoeae. They can also be used in eye care solutions and as  
 CC preservatives for food. The protegrins are more effective under  
 CC physiological conditions (e.g. in the presence of serum) than certain  
 CC antibiotics and are non-toxic to the cells of higher organisms. (Updated  
 CC on 25-MAR-2003 to correct PA field.)  
 XX SQ Sequence 18 AA;  
 Query Match 71.4%; Score 65; DB 2; Length 18;  
 Best Local Similarity 66.7%; Pred. No. 0.0028;  
 Matches 12; Conservative 2; Mismatches 4; Indels 0; Gaps 0;  
 QY 1 RGRGLSYRRRSTSTGR 18  
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 Db 1 RGRGLCYARRRFAVCVGR 18  
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 ADL18459  
 ID ADL18459 standard; peptide; 18 AA.  
 XX AC ADL18459;  
 XX DT 06-MAY-2004 (first entry)  
 XX DE Antimicrobial protegrin peptide IB-288.  
 XX virucide; antimicrobial; peptide therapy; recombinant peptide compound;  
 KW antiviral; viral infection; microbial infection; endotoxin inactivation;  
 KW eye care; contact lens solution; topical composition;  
 KW pharmaceutical composition; sexually transmitted disease; STD; protegrin.  
 XX OS Synthetic.  
 XX

PN US6653442-B1.  
 XX PD 25-NOV-2003.  
 XX PF 30-AUG-1999; 99US-00385328.  
 XX PR 20-JUL-1993; 93US-00093926.  
 XX PR 26-JUL-1993; 93US-00095769.  
 XX PR 13-JAN-1994; 94US-00182483.  
 XX PR 17-MAY-1994; 94US-00243879.  
 XX PR 07-JUL-1995; 95US-00499523.  
 XX PR 24-MAY-1996; 96WO-US007594.  
 XX PR 28-OCT-1996; 96US-00741860.  
 XX PR 03-AUG-1998; 98US-00128345.  
 XX PA (INTR-) INTRABIOTICS PHARM INC.  
 XX PI Chang CC, Gu CL, Chen J, Steinberg DA, Lehrer RI, Harwig SSL;  
 PI Kokryakov VN;  
 XX WPI; 2004-068297/07.  
 XX DR New peptide in its N-terminal acylated or C-terminal amidated or  
 PT esterified form in linear or cysteine-bridged form, useful for treating  
 PT sexually transmitted diseases and as preservatives.  
 XX PS Claim 1; SEQ ID NO 99; 84pp; English.  
 XX CC The invention describes a purified and isolated or recombinantly produced  
 CC peptide compound selected from any of the 43 fully defined sequences of  
 CC 16-18 amino acids, given in the specification, or its N-terminal acylated  
 CC or C-terminal amidated or esterified forms in linear or cysteine-bridged  
 CC form. Also described are: a pharmaceutical composition for antimicrobial  
 CC or antiviral use, comprising any of the peptides cited above in admixture  
 CC with at least one excipient; and a composition for application to plants  
 CC or plant environments for conferring resistance to microbial or viral  
 CC infections in plants comprising any of the peptides cited above in  
 CC admixture with at least one diluent. The peptides are useful as  
 CC preservatives and in preventing, treating or ameliorating viral or  
 CC microbial infections in animals and plants, and in inactivating  
 CC endotoxins. They are particularly useful in eye care, such as in contact  
 CC lens solutions, and in topical and pharmaceutical compositions for  
 CC treating sexually transmitted diseases (STDs). This is the amino acid  
 CC sequence of an antimicrobial protegrin peptide of the invention.  
 XX SQ Sequence 18 AA;  
 Query Match 71.4%; Score 65; DB 8; Length 18;  
 Best Local Similarity 66.7%; Pred. No. 0.0028;  
 Matches 12; Conservative 2; Mismatches 4; Indels 0; Gaps 0;  
 QY 1 RGRGLSYRRRSTSTGR 18  
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 Db 1 RGRGLCYARRRFAVCVGR 18  
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 ADL18460  
 ID ADL18460 standard; peptide; 18 AA.  
 XX AC ADL18460;  
 XX DT 06-MAY-2004 (first entry)  
 XX DE Antimicrobial protegrin peptide IB-289.  
 XX virucide; antimicrobial; peptide therapy; recombinant peptide compound;  
 KW antiviral; viral infection; microbial infection; endotoxin inactivation;  
 KW eye care; contact lens solution; topical composition;  
 KW pharmaceutical composition; sexually transmitted disease; STD; protegrin.  
 XX OS Synthetic.  
 XX

FH Key Location/Qualifiers  
FT Modified-site 18  
FT /label= OTHER  
FT /note= "OTHER= C-terminal amidation"  
XX  
XX US6653442-B1.  
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PD 25-NOV-2003.  
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XX 30-AUG-1999; 99US-00385328.  
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XX 20-JUL-1993; 93US-00093926.  
PR 26-JUL-1993; 93US-00095769.  
PR 13-JAN-1994; 94US-00182483.  
PR 17-MAY-1994; 94US-00243879.  
PR 07-JUL-1995; 95US-00499523.  
PR 24-MAY-1996; 96WO-US007594.  
PR 28-OCT-1996; 96US-00741860.  
PR 03-AUG-1998; 98US-00128345.  
XX  
XX (INTR-) INTRABIOTICS PHARM INC.  
XX  
XX Chang CC, Gu CL, Chen J, Steinberg DA, Lehrer RI, Harwig SSL;  
PI Kokryakov VN;  
XX  
XX WPI; 2004-068297/07.  
DR  
XX  
XX New peptide in its N-terminal acylated or C-terminal amidated or  
PT esterified form in linear or cysteine-bridged form, useful for treating  
PT sexually transmitted diseases and as preservatives.  
XX  
XX Claim 1; SEQ ID NO 100; 84pp; English.  
PS  
XX  
XX The invention describes a purified and isolated or recombinantly produced  
CC peptide compound selected from any of the 43 fully defined sequences of  
CC 16-18 amino acids, given in the specification, or its N-terminal acylated  
CC or C-terminal amidated or esterified forms in linear or cysteine-bridged  
CC form. Also described are: a pharmaceutical composition for antimicrobial  
CC or antiviral use, comprising any of the peptides cited above in admixture  
CC with at least one excipient; and a composition for application to plants  
CC or plant environments for conferring resistance to microbial or viral  
CC infections in plants comprising any of the peptides cited above in  
CC admixture with at least one diluent. The peptides are useful as  
CC preservatives and in preventing, treating or ameliorating viral or  
CC microbial infections in animals and plants, and in inactivating  
CC endotoxins. They are particularly useful in eye care, such as in contact  
CC lens solutions, and in topical and pharmaceutical compositions for  
CC treating sexually transmitted diseases (STDs). This is the amino acid  
CC sequence of an antimicrobial protegrin peptide of the invention.  
XX  
SQ Sequence 18 AA;  
Query Match 71.4%; Score 65; DB 8; Length 18;  
Best Local Similarity 66.7%; Pred. No. 0.0028;  
Matches 12; Conservative 2; Mismatches 4; Indels 0; Gaps 0;  
QY 1 RGRGLYSRRRFFSTGTGR 18  
Db 1 RGRGLCYARRRFFAVCVGR 18  
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Job time : 199 secs



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OM protein - protein search, using sw model

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Title: US-09-857-000A-11

Perfect score: 91

Sequence: 1 RGGLSVSRRRRPFSTSTGR 18

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Total number of hits satisfying chosen parameters: 650591

Minimum DB seq length: 0

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Listing first 100 summaries

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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

#### SUMMARIES

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Sequence 107, App  
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Sequence 2, Appl  
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Sequence 77, Appl  
Sequence 41, Appl  
Sequence 26, Appl  
Sequence 25, Appl  
Sequence 46, Appl  
Sequence 55, Appl

100 56 61.5 18 1 US-08-499-523-57 Sequence 57, Appl

## ALIGNMENTS

## RESULT 1

US-10-144-549-17  
; Sequence 17, Application US/10144549  
; Patent No. 6835810  
; GENERAL INFORMATION:  
; APPLICANT: GenShuttle Biopharm, Inc.  
; APPLICANT: Hwu, Paul L.  
; TITLE OF INVENTION: A NEW FUSION PROTEIN FOR USE AS VECTOR  
; FILE REFERENCE: MEHB 02-340  
; CURRENT APPLICATION NUMBER: US/10/144,549  
; CURRENT FILING DATE: 2002-05-13  
; NUMBER OF SEQ ID NOS: 31  
; SOFTWARE: PatentIn version 3.1  
; SEQ ID NO 17  
; LENGTH: 18  
; TYPE: PRT  
; ORGANISM: Artificial Sequence  
; FEATURE:  
; OTHER INFORMATION: Membrane fusion sequence.  
; NAME/KEY: MISC FEATURE  
; OTHER INFORMATION: Synthetic sequence from protegrins/procine leukocyte.  
US-10-144-549-17

Query Match 100.0%; Score 91; DB 2; Length 18;  
Best Local Similarity 100.0%; Pred. No. 5.9e-08;  
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 RGGRLSYRRRFSTSTGR 18  
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Db 1 RGGRLSYRRRFSTSTGR 18

## RESULT 2

US-09-810-601B-42  
; Sequence 42, Application US/09810601B  
; Patent No. 6831059  
; GENERAL INFORMATION:  
; APPLICANT: Allergan Sales, Inc.  
; APPLICANT: Donovan, Stephen  
; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR TREATING GONADOTROPHIN RELATED ILLNE  
; FILE REFERENCE: D-2947-CIP  
; CURRENT APPLICATION NUMBER: US/09/810,601B  
; CURRENT FILING DATE: 2001-03-15  
; PRIOR APPLICATION NUMBER: 09/692,811  
; PRIOR FILING DATE: 2000-10-20  
; NUMBER OF SEQ ID NOS: 52  
; SOFTWARE: PatentIn version 3.1  
; SEQ ID NO 42  
; LENGTH: 18  
; TYPE: PRT  
; ORGANISM: Artificial Sequence  
; FEATURE:  
; OTHER INFORMATION: Membrane Translocation Peptide  
US-09-810-601B-42

Query Match 87.9%; Score 80; DB 2; Length 18;  
Best Local Similarity 88.9%; Pred. No. 3.3e-06;  
Matches 16; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 1 RGGRLSYRRRFSTSTGR 18  
|||||:|||||  
Db 1 RGGRLSYRRRFSTSTGR 18

## RESULT 3

US-09-385-328-93

; Sequence 93, Application US/09385328  
; Patent No. 6653442  
; GENERAL INFORMATION:  
; APPLICANT: Chang, Conway C.  
; APPLICANT: Gu, Chee L.  
; APPLICANT: Chen, Jie  
; APPLICANT: Steinberg, Deborah A.  
; APPLICANT: Lehrer, Robert I.  
; APPLICANT: Harwig, Sylvia S. L.  
; APPLICANT: Kokryakov, Vladimir N.  
; TITLE OF INVENTION: PROTEGRINS  
; FILE REFERENCE: 8067-0067-999  
; CURRENT APPLICATION NUMBER: US/09/385,328  
; CURRENT FILING DATE: 1999-08-30  
; PRIOR APPLICATION NUMBER: US 09/128,345  
; PRIOR FILING DATE: 1998-08-03  
; PRIOR APPLICATION NUMBER: US 08/741,860  
; PRIOR FILING DATE: 1996-10-28  
; NUMBER OF SEQ ID NOS: 125  
; SOFTWARE: FastSeq for Windows Version 4.0  
; SEQ ID NO 93  
; LENGTH: 18  
; TYPE: PRT  
; ORGANISM: Artificial Sequence  
; FEATURE:  
; OTHER INFORMATION: Synthetic peptide  
; NAME/KEY: AMIDATION  
; LOCATION: 18  
; OTHER INFORMATION: C-terminal amidation  
US-09-385-328-93

Query Match 73.6%; Score 67; DB 2; Length 18;  
Best Local Similarity 66.7%; Pred. No. 0.00038;  
Matches 12; Conservative 4; Mismatches 2; Indels 0; Gaps 0;

QY 1 RGGRLSYRRRFSTSTGR 18  
|||||:|||||  
Db 1 RGGRLAYARRFAVWGR 18

## RESULT 4

US-08-984-294-6  
; Sequence 6, Application US/08984294  
; Patent No. 6043220  
; GENERAL INFORMATION:  
; APPLICANT: Chang, Conway C.  
; APPLICANT: Chen, Jie  
; APPLICANT: Lehrer, Robert I.  
; TITLE OF INVENTION: THREONINE-CONTAINING PROTEGRINS  
; NUMBER OF SEQUENCES: 19  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: Pennie & Edmonds LLP  
; STREET: 1155 Avenue of The Americas  
; CITY: New York  
; STATE: NY  
; COUNTRY: USA  
; ZIP: 10036-2811  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Diskette  
; OPERATING SYSTEM: DOS  
; SOFTWARE: FastSeq Version 2.0  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/08/984,294  
; FILING DATE: 03-DEC-1997  
; CLASSIFICATION: 530  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER:  
; FILING DATE:  
; ATTORNEY/AGENT INFORMATION:  
; NAME: Coruzzi, Laura A  
; REGISTRATION NUMBER: 30,742  
; REFERENCE/DOCKET NUMBER: 008067-0049-999

TELECOMMUNICATION INFORMATION:  
TELEPHONE: 650-493-4935  
TELEFAX: 650-493-5556  
TELEX: 66141 PENNIE  
INFORMATION FOR SEQ ID NO: 6:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 18 amino acids  
TYPE: amino acid  
STRANDEDNESS: single  
TOPOLOGY: linear  
MOLECULE TYPE: No. 6043220e  
US-08-984-294-6

Query Match 72.5%; Score 66; DB 2; Length 18;  
Best Local Similarity 72.2%; Pred. No. 0.00055;  
Matches 13; Conservative 0; Mismatches 5; Indels 0; Gaps 0;

QY 1 RGGRLSYRRRFFSTGTGR 18  
DB 1 RGGRLCYRRRFFCTGVR 18

## RESULT 5

US-08-984-294-8  
Sequence 8, Application US/08984294  
Patent No. 6043220  
GENERAL INFORMATION:  
APPLICANT: Chang, Conway C.  
APPLICANT: Chen, Jie  
APPLICANT: Lehrer, Robert I.  
TITLE OF INVENTION: THREONINE-CONTAINING PROTEGRINS  
NUMBER OF SEQUENCES: 19

CORRESPONDENCE ADDRESS:  
ADDRESSEE: Pennie & Edmonds LLP  
STREET: 1155 Avenue of The Americas  
CITY: New York  
STATE: NY  
COUNTRY: USA

ZIP: 10036-2811  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Diskette  
COMPUTER: IBM Compatible  
OPERATING SYSTEM: DOS  
SOFTWARE: FastSeq Version 2.0  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/984,294  
FILING DATE: 03-DEC-1997  
CLASSIFICATION: 530  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER:  
FILING DATE:

ATTORNEY/AGENT INFORMATION:  
NAME: Coruzzi, Laura A  
REGISTRATION NUMBER: 30,742  
REFERENCE/DOCKET NUMBER: 008067-0049-999  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: 650-493-4935  
TELEFAX: 650-493-5556  
TELEX: 66141 PENNIE

INFORMATION FOR SEQ ID NO: 8:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 18 amino acids  
TYPE: amino acid  
STRANDEDNESS: single  
TOPOLOGY: linear  
MOLECULE TYPE: No. 6043220e  
US-08-984-294-8

Query Match 72.5%; Score 66; DB 2; Length 18;  
Best Local Similarity 72.2%; Pred. No. 0.00055;  
Matches 13; Conservative 0; Mismatches 5; Indels 0; Gaps 0;

QY 1 RGGRLSYRRRFFSTGTGR 18

DB 1 RGGRLCYRRRFFCTGVR 18

## RESULT 6

US-08-499-523-63  
Sequence 63, Application US/08499523  
Patent No. 5804558  
GENERAL INFORMATION:  
APPLICANT: LEHRER, ROBERT I.  
APPLICANT: HARWIG, SYLVIA S.L.  
APPLICANT: KOKRYAKOV, VLADIMIR N.  
TITLE OF INVENTION: PROTEGRINS  
NUMBER OF SEQUENCES: 76  
CORRESPONDENCE ADDRESS:

ADDRESSEE: MORRISON & FOERSTER  
STREET: 2000 Pennsylvania Ave. N.W., Ste. 5500  
CITY: Washington  
STATE: DC  
COUNTRY: USA  
ZIP: 20006-1812

COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: Patent In Release #1.0, Version #1.30  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/499,523

FILING DATE: 07-JUL-1995  
CLASSIFICATION: 514

ATTORNEY/AGENT INFORMATION:  
NAME: MURASHIGE, KATE H.  
REGISTRATION NUMBER: 29,959  
REFERENCE/DOCKET NUMBER: 2000-0540.24  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (202) 887-1500  
TELEFAX: (202) 887-0763  
TELEX: 90-4030

INFORMATION FOR SEQ ID NO: 63:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 18 amino acids  
TYPE: amino acid  
STRANDEDNESS: single  
TOPOLOGY: linear  
FEATURE:  
NAME/KEY: Modified-site  
LOCATION: group(6, 8, 13, 15)  
OTHER INFORMATION: /note= "X is a hydrophobic, a  
OTHER INFORMATION: small, or a large polar amino acid"  
US-08-499-523-63

Query Match 71.4%; Score 65; DB 1; Length 18;  
Best Local Similarity 66.7%; Pred. No. 0.0008; 6; Indels 0; Gaps 0;  
Matches 12; Conservative 0; Mismatches 6; Indels 0; Gaps 0;

QY 1 RGGRLSYRRRFFSTGTGR 18

DB 1 RGGRLXXRRRFFXVXVGR 18

## RESULT 7

US-08-499-523-67  
Sequence 67, Application US/08499523  
Patent No. 5804558  
GENERAL INFORMATION:

APPLICANT: LEHRER, ROBERT I.  
APPLICANT: HARWIG, SYLVIA S.L.  
APPLICANT: KOKRYAKOV, VLADIMIR N.  
TITLE OF INVENTION: PROTEGRINS  
NUMBER OF SEQUENCES: 76  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: MORRISON & FOERSTER  
STREET: 2000 Pennsylvania Ave. N.W., Ste. 5500

QY 1 RGGRLSYRRRFFSTGTGR 18

;  
; CITY: Washington  
; STATE: DC  
; COUNTRY: USA  
; ZIP: 20006-1812  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Floppy disk  
; COMPUTER: IBM PC compatible  
; OPERATING SYSTEM: PC-DOS/MS-DOS  
; SOFTWARE: PatentIn Release #1.0, Version #1.30  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/08/499,523  
; FILING DATE: 07-JUL-1995  
; CLASSIFICATION: 514  
; ATTORNEY/AGENT INFORMATION:  
; NAME: MURASHIGE, KATE H.  
; REGISTRATION NUMBER: 29,959  
; REFERENCE/DOCKET NUMBER: 2000-0540.24  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: (202) 887-1500  
; TELEFAX: (202) 887-0763  
; TELEX: 90-4030  
; INFORMATION FOR SEQ ID NO: 67:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 18 amino acids  
; TYPE: amino acid  
; STRANDEDNESS: single  
; TOPOLOGY: linear  
; FEATURE:  
; NAME/KEY: Modified-site  
; LOCATION: group(6, 8, 13, 15)  
; OTHER INFORMATION: /note= "X is a hydrophobic, a  
; OTHER INFORMATION: small, or a large polar amino acid"  
; US-08-499-523-67

Query Match 71.4%; Score 65; DB 1; Length 18;  
Best Local Similarity 66.7%; Pred. No. 0.0008; 6; Indels 0; Gaps 0;  
Matches 12; Conservative 0; Mismatches 6; Indels 0; Gaps 0;

QY 1 RGGRLSYRRRFFSTGTGR 18  
||||| :||| :||  
Db 1 RGGRLXYRRRFXVXVGR 18  
RESULT 8  
US-08-752-852A-230  
; Sequence 230, Application US/08752852A  
; Patent No. 5994306  
; GENERAL INFORMATION:  
; APPLICANT: Chang, Conway  
; APPLICANT: Gu, Chee-liang  
; APPLICANT: Chen, Jie  
; APPLICANT: Steinberg, Deborah  
; APPLICANT: Lehrer, Robert  
; APPLICANT: Harwig, Sylvia  
; TITLE OF INVENTION: FINE-TUNED PROTEGRINS  
; NUMBER OF SEQUENCES: 242  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: PENNIE & EDMONDS LLP  
; STREET: 1155 Avenue of the Americas  
; CITY: New York  
; STATE: NY  
; COUNTRY: USA  
; ZIP: 10036-2711  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Diskette  
; COMPUTER: IBM Compatible  
; OPERATING SYSTEM: DOS  
; SOFTWARE: FastSeq Version 2.0  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/08/752,852A  
; FILING DATE: 21-NOV-1996  
; CLASSIFICATION: 435  
; PRIOR APPLICATION DATA:

;  
; APPLICATION NUMBER:  
; FILING DATE:  
; ATTORNEY/AGENT INFORMATION:  
; NAME: Coruzzi, Laura A.  
; REGISTRATION NUMBER: 30,742  
; REFERENCE/DOCKET NUMBER: 8067-034-999  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: 212-790-9090  
; TELEFAX: 212-869-9741  
; TELEX: 66141  
; INFORMATION FOR SEQ ID NO: 230:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 18 amino acids  
; TYPE: amino acid  
; STRANDEDNESS: unknown  
; TOPOLOGY: unknown  
; MOLECULE TYPE: peptide  
; US-08-752-852A-230  
Query Match 71.4%; Score 65; DB 1; Length 18;  
Best Local Similarity 66.7%; Pred. No. 0.0008; 4; Indels 0; Gaps 0;  
Matches 12; Conservative 2; Mismatches 4; Indels 0; Gaps 0;  
QY 1 RGGRLSYRRRFFSTGTGR 18  
||||| :||| :||  
Db 1 RGGRLCYARRRFAVCVGR 18  
RESULT 9  
US-09-128-345-63  
; Sequence 63, Application US/09128345  
; Patent No. 6159936  
; GENERAL INFORMATION:  
; APPLICANT: LEHRER, ROBERT I.  
; APPLICANT: HARWIG, SYLVIA S.L.  
; APPLICANT: KOKRYAKOV, VLADIMIR N.  
; TITLE OF INVENTION: PROTEGRINS  
; NUMBER OF SEQUENCES: 76  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: PENNIE & EDMONDS LLP  
; STREET: 1155 Avenue of the Americas  
; CITY: New York  
; STATE: New York  
; COUNTRY: USA  
; ZIP: 10036-2711  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Floppy disk  
; COMPUTER: IBM PC compatible  
; OPERATING SYSTEM: PC-DOS/MS-DOS  
; SOFTWARE: PatentIn Release #1.0, Version #1.30  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/09/128,345  
; FILING DATE: 03-AUG-1998  
; CLASSIFICATION: 514  
; ATTORNEY/AGENT INFORMATION:  
; NAME: Coruzzi, Laura A.  
; REGISTRATION NUMBER: 30,742  
; REFERENCE/DOCKET NUMBER: 8067-0054-999  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: (212) 790-9090  
; TELEFAX: (212) 869-9741  
; TELEX: 66141 PENNIE  
; INFORMATION FOR SEQ ID NO: 63:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 18 amino acids  
; TYPE: amino acid  
; STRANDEDNESS: single  
; TOPOLOGY: linear  
; FEATURE:  
; NAME/KEY: Modified-site  
; LOCATION: group(6, 8, 13, 15)  
; OTHER INFORMATION: /note= "X is a hydrophobic, a  
; OTHER INFORMATION: small, or a large polar amino acid"

## US-09-128-345-63

Query Match 71.4%; Score 65; DB 2; Length 18;  
Best Local Similarity 66.7%; Pred. No. 0.0008;  
Matches 12; Conservative 0; Mismatches 6; Indels 0; Gaps 0;

Qy 1 RGGRLSYRRRPFSTGTGR 18  
Db 1 RGGRLXYRRRPFVXVGR 18

## RESULT 10

US-09-128-345-67  
; Sequence 67, Application US/09128345  
; Patent No. 6159936  
; GENERAL INFORMATION:  
; APPLICANT: LEHRER, ROBERT I.  
; APPLICANT: HARWIG, SYLVIA S. L.  
; APPLICANT: KOKRYAKOV VLADIMIR N.  
; TITLE OF INVENTION: PROTEGRINS  
; NUMBER OF SEQUENCES: 76  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: PENNIE & EDMONDS LLP  
; STREET: 1155 Avenue of the Americas  
; CITY: New York  
; STATE: New York  
; COUNTRY: USA  
; ZIP: 10036-2711  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Floppy disk  
; COMPUTER: IBM PC compatible  
; OPERATING SYSTEM: PC-DOS/MS-DOS  
; SOFTWARE: PatentIn Release #1.0, Version #1.30  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/09/128,345  
; FILING DATE: 03-AUG-1998  
; CLASSIFICATION: 514  
; ATTORNEY/AGENT INFORMATION:  
; NAME: Coruzzi, Laura, A.  
; REGISTRATION NUMBER: 30,742  
; REFERENCE/DOCKET NUMBER: 8067-0054-999  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: (212) 790-9090  
; TELEFAX: (212) 869-9741  
; TELEX: 66141 PENNIE  
; INFORMATION FOR SEQ ID NO: 67:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 18 amino acids  
; TYPE: amino acid  
; STRANDEDNESS: single  
; TOPOLOGY: linear  
; FEATURE:  
; NAME/KEY: Modified-site  
; LOCATION: group(6, 8, 13, 15)  
; OTHER INFORMATION: /note= "X is a hydrophobic, a  
; OTHER INFORMATION: small, or a large polar amino acid"

US-09-128-345-67  
Query Match 71.4%; Score 65; DB 2; Length 18;  
Best Local Similarity 66.7%; Pred. No. 0.0008;  
Matches 12; Conservative 0; Mismatches 6; Indels 0; Gaps 0;

Qy 1 RGGRLSYRRRPFSTGTGR 18  
Db 1 RGGRLXYRRRPFVXVGR 18

## RESULT 11

US-09-385-328-99  
; Sequence 99, Application US/09385328  
; Patent No. 6653442  
; GENERAL INFORMATION:  
; APPLICANT: Chang, Conway C.

; APPLICANT: Gu, Chee L.  
; APPLICANT: Chen, Jie  
; APPLICANT: Steinberg, Deborah A.  
; APPLICANT: Lehrer, Robert I.  
; APPLICANT: Harwig, Sylvia S. L.  
; APPLICANT: Kokryakov, Vladimir N.  
; TITLE OF INVENTION: PROTEGRINS  
; FILE REFERENCE: 8067-0067-999  
; CURRENT APPLICATION NUMBER: US/09/385,328  
; CURRENT FILING DATE: 1999-08-30  
; PRIOR APPLICATION NUMBER: US 09/128,345  
; PRIOR FILING DATE: 1998-08-03  
; PRIOR APPLICATION NUMBER: US 08/741,860  
; PRIOR FILING DATE: 1996-10-28  
; NUMBER OF SEQ ID NOS: 125  
; SOFTWARE: FastSeq for Windows Version 4.0  
; SEQ ID NO 99  
; LENGTH: 18  
; TYPE: PRT  
; ORGANISM: Artificial Sequence  
; FEATURE:  
; OTHER INFORMATION: Synthetic peptide  
US-09-385-328-99

Query Match 71.4%; Score 65; DB 2; Length 18;  
Best Local Similarity 66.7%; Pred. No. 0.0008;  
Matches 12; Conservative 2; Mismatches 4; Indels 0; Gaps 0;

Qy 1 RGGRLSYRRRPFSTGTGR 18  
Db 1 RGGRLCYARRRFAVCVGR 18

## RESULT 12

US-09-385-328-100  
; Sequence 100, Application US/09385328  
; Patent No. 6653442  
; GENERAL INFORMATION:  
; APPLICANT: Chang, Conway C.  
; APPLICANT: Gu, Chee L.  
; APPLICANT: Chen, Jie  
; APPLICANT: Steinberg, Deborah A.  
; APPLICANT: Lehrer, Robert I.  
; APPLICANT: Harwig, Sylvia S. L.  
; APPLICANT: Kokryakov, Vladimir N.  
; TITLE OF INVENTION: PROTEGRINS  
; FILE REFERENCE: 8067-0067-999  
; CURRENT APPLICATION NUMBER: US/09/385,328  
; CURRENT FILING DATE: 1999-08-30  
; PRIOR APPLICATION NUMBER: US 09/128,345  
; PRIOR FILING DATE: 1998-08-03  
; PRIOR APPLICATION NUMBER: US 08/741,860  
; PRIOR FILING DATE: 1996-10-28  
; NUMBER OF SEQ ID NOS: 125  
; SOFTWARE: FastSeq for Windows Version 4.0  
; SEQ ID NO 100  
; LENGTH: 18  
; TYPE: PRT  
; ORGANISM: Artificial Sequence  
; FEATURE:  
; OTHER INFORMATION: Synthetic peptide  
; NAME/KEY: AMIDATION  
; LOCATION: 18  
; OTHER INFORMATION: C-terminal amidation  
US-09-385-328-100

Query Match 71.4%; Score 65; DB 2; Length 18;  
Best Local Similarity 66.7%; Pred. No. 0.0008;  
Matches 12; Conservative 2; Mismatches 4; Indels 0; Gaps 0;

Qy 1 RGGRLSYRRRPFSTGTGR 18  
Db 1 RGGRLCYARRRFAVCVGR 18

```
RESULT 13
US-09-385-328-111
; Sequence 91, Application US/09385328
; Patent No. 6653442
; GENERAL INFORMATION:
; APPLICANT: Chang, Conway C.
; APPLICANT: Gu, Chee L.
; APPLICANT: Steinberg, Deborah A.
; APPLICANT: Lehrer, Robert I.
; APPLICANT: Harwig, Sylvia S. L.
; APPLICANT: Kokryakov, Vladimir N.
; TITLE OF INVENTION: PROTEGRINS
; FILE REFERENCE: 8067-0067-999
; CURRENT APPLICATION NUMBER: US/09/385,328
; CURRENT FILING DATE: 1999-08-30
; PRIOR APPLICATION NUMBER: US 09/128,345
; PRIOR FILING DATE: 1998-08-03
; PRIOR APPLICATION NUMBER: US 08/741,860
; PRIOR FILING DATE: 1996-10-28
; NUMBER OF SEQ ID NOS: 125
; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 111
; LENGTH: 18
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Synthetic peptide
; NAME/KEY: AMIDATION
; LOCATION: 18
; OTHER INFORMATION: C-terminal amidation
; NAME/KEY: SITE
; LOCATION: 6, 8, 13, 15
; OTHER INFORMATION: Xaa = hydrophobic, small or large polar amino acid
US-09-385-328-111

Query Match          71.4%; Score 65; DB 2; Length 18;
Best Local Similarity 66.7%; Pred. No. 0.0008;
Matches 12; Conservative 0; Mismatches 6; Indels 0; Gaps 0;

QY      1 RGGRLSYRRRSTSTGR 18
DB      1 RGGRLXYRRRFXVXVGR 18

RESULT 14
US-09-385-328-91
; Sequence 91, Application US/09385328
; Patent No. 6653442
; GENERAL INFORMATION:
; APPLICANT: Chang, Conway C.
; APPLICANT: Chen, Jie
; APPLICANT: Steinberg, Deborah A.
; APPLICANT: Lehrer, Robert I.
; APPLICANT: Harwig, Sylvia S. L.
; APPLICANT: Kokryakov, Vladimir N.
; TITLE OF INVENTION: PROTEGRINS
; FILE REFERENCE: 8067-0067-999
; CURRENT APPLICATION NUMBER: US/09/385,328
; CURRENT FILING DATE: 1999-08-30
; PRIOR APPLICATION NUMBER: US 09/128,345
; PRIOR FILING DATE: 1998-08-03
; PRIOR APPLICATION NUMBER: US 08/741,860
; PRIOR FILING DATE: 1996-10-28
; NUMBER OF SEQ ID NOS: 125
; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 91
; LENGTH: 18
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Synthetic peptide
; NAME/KEY: AMIDATION
; LOCATION: 18
; OTHER INFORMATION: C-terminal amidation
; NAME/KEY: SITE
; LOCATION: 18
; OTHER INFORMATION: C-terminal amidation
US-09-385-328-92
; Sequence 92, Application US/09385328
; Patent No. 6653442
; GENERAL INFORMATION:
; APPLICANT: Chang, Conway C.
; APPLICANT: Gu, Chee L.
; APPLICANT: Chen, Jie
; APPLICANT: Steinberg, Deborah A.
; APPLICANT: Lehrer, Robert I.
; APPLICANT: Harwig, Sylvia S. L.
; APPLICANT: Kokryakov, Vladimir N.
; TITLE OF INVENTION: PROTEGRINS
; FILE REFERENCE: 8067-0067-999
; CURRENT APPLICATION NUMBER: US/09/385,328
; CURRENT FILING DATE: 1999-08-30
; PRIOR APPLICATION NUMBER: US 09/128,345
; PRIOR FILING DATE: 1998-08-03
; PRIOR APPLICATION NUMBER: US 08/741,860
; PRIOR FILING DATE: 1996-10-28
; NUMBER OF SEQ ID NOS: 125
; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 92
; LENGTH: 18
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Synthetic peptide
; NAME/KEY: AMIDATION
; LOCATION: 18
; OTHER INFORMATION: C-terminal amidation
US-09-385-328-92

Query Match          70.3%; Score 64; DB 2; Length 18;
Best Local Similarity 61.1%; Pred. No. 0.0012;
Matches 11; Conservative 5; Mismatches 2; Indels 0; Gaps 0;

QY      1 RGGRLSYRRRSTSTGR 18
DB      1 RGGRLAYARRRWAFAVGR 18

RESULT 16
US-08-499-523-53
; Sequence 53, Application US/08499523
; Patent No. 5804558
; GENERAL INFORMATION:
; APPLICANT: LEHRER, ROBERT I.
; APPLICANT: HARWIG, SYLVIA S.L.
; APPLICANT: KOKRYAKOV, VLADIMIR N.
; TITLE OF INVENTION: PROTEGRINS
; NUMBER OF SEQUENCES: 76
; CORRESPONDENCE ADDRESS:
; ADDRESSSEE: MORRISON & FOERSTER
; STREET: 2000 Pennsylvania Ave. N.W., Ste. 5500
; CITY: Washington
; STATE: DC
```

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; FEATURE:
; OTHER INFORMATION: Synthetic peptide
; NAME/KEY: AMIDATION
; LOCATION: 18
; OTHER INFORMATION: C-terminal amidation
US-09-385-328-91

Query Match          70.3%; Score 64; DB 2; Length 18;
Best Local Similarity 61.1%; Pred. No. 0.0012;
Matches 11; Conservative 5; Mismatches 2; Indels 0; Gaps 0;

QY      1 RGGRLSYRRRSTSTGR 18
DB      1 RGGRLAYARRRWAFAVGR 18

RESULT 15
US-09-385-328-92
; Sequence 92, Application US/09385328
; Patent No. 6653442
; GENERAL INFORMATION:
; APPLICANT: Chang, Conway C.
; APPLICANT: Gu, Chee L.
; APPLICANT: Chen, Jie
; APPLICANT: Steinberg, Deborah A.
; APPLICANT: Lehrer, Robert I.
; APPLICANT: Harwig, Sylvia S. L.
; APPLICANT: Kokryakov, Vladimir N.
; TITLE OF INVENTION: PROTEGRINS
; FILE REFERENCE: 8067-0067-999
; CURRENT APPLICATION NUMBER: US/09/385,328
; CURRENT FILING DATE: 1999-08-30
; PRIOR APPLICATION NUMBER: US 09/128,345
; PRIOR FILING DATE: 1998-08-03
; PRIOR APPLICATION NUMBER: US 08/741,860
; PRIOR FILING DATE: 1996-10-28
; NUMBER OF SEQ ID NOS: 125
; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 92
; LENGTH: 18
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Synthetic peptide
; NAME/KEY: AMIDATION
; LOCATION: 18
; OTHER INFORMATION: C-terminal amidation
US-09-385-328-92

Query Match          70.3%; Score 64; DB 2; Length 18;
Best Local Similarity 61.1%; Pred. No. 0.0012;
Matches 11; Conservative 5; Mismatches 2; Indels 0; Gaps 0;

QY      1 RGGRLSYRRRSTSTGR 18
DB      1 RGGRLAYARRRWAFAVGR 18

RESULT 16
US-08-499-523-53
; Sequence 53, Application US/08499523
; Patent No. 5804558
; GENERAL INFORMATION:
; APPLICANT: LEHRER, ROBERT I.
; APPLICANT: HARWIG, SYLVIA S.L.
; APPLICANT: KOKRYAKOV, VLADIMIR N.
; TITLE OF INVENTION: PROTEGRINS
; NUMBER OF SEQUENCES: 76
; CORRESPONDENCE ADDRESS:
; ADDRESSSEE: MORRISON & FOERSTER
; STREET: 2000 Pennsylvania Ave. N.W., Ste. 5500
; CITY: Washington
; STATE: DC
```

```

; COUNTRY: USA
; ZIP: 20006-1812
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/499,523
; FILING DATE: 07-JUL-1995
; CLASSIFICATION: 514
; ATTORNEY/AGENT INFORMATION:
; NAME: MURASHIGE, KATE H.
; REGISTRATION NUMBER: 29,959
; REFERENCE/DOCKET NUMBER: 2000-0540.24
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (202) 887-1500
; TELEFAX: (202) 887-0763
; TELEX: 90-4030
; INFORMATION FOR SEQ ID NO: 53:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 18 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; FEATURE:
; NAME/KEY: Disulfide-bond
; LOCATION: 8..13
; FEATURE:
; NAME/KEY: Modified-site
; LOCATION: group(6, 15)
; OTHER INFORMATION: /note= "X is a hydrophobic, a
; OTHER INFORMATION: small, or a large polar amino acid"
; US-08-499-523-53

Query Match 69.2%; Score 63; DB 1; Length 18;
Best Local Similarity 66.7%; Pred. No. 0.0017;
Matches 12; Conservative 0; Mismatches 6; Indels 0; Gaps 0;

Qy 1 RGGRLSYRRRFFSTGSR 18
   ||||| |||||
Db 1 RGGRLCYRRRFFCVXGR 18

RESULT 17
US-08-499-523-58
; Sequence 58, Application US/08499523
; Patent No. 5804558
; GENERAL INFORMATION:
; APPLICANT: LEHRER, ROBERT I.
; APPLICANT: HARWIG, SYLVIA S.L.
; APPLICANT: KOKRYAKOV, VLADIMIR N.
; TITLE OF INVENTION: PROTEGRINS
; NUMBER OF SEQUENCES: 76
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: MORRISON & FOERSTER
; STREET: 2000 Pennsylvania Ave. N.W., Ste. 5500
; CITY: Washington
; STATE: DC
; COUNTRY: USA
; ZIP: 20006-1812
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/499,523
; FILING DATE: 07-JUL-1995
; CLASSIFICATION: 514
; ATTORNEY/AGENT INFORMATION:
; NAME: MURASHIGE, KATE H.
; REGISTRATION NUMBER: 29,959

```

```

; REFERENCE/DOCKET NUMBER: 2000-0540.24
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (202) 887-1500
; TELEFAX: (202) 887-0763
; TELEX: 90-4030
; INFORMATION FOR SEQ ID NO: 58:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 18 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; FEATURE:
; NAME/KEY: Disulfide-bond
; LOCATION: 6..15
; FEATURE:
; NAME/KEY: Modified-site
; LOCATION: group(8, 13)
; OTHER INFORMATION: /note= "X is a hydrophobic, a
; OTHER INFORMATION: small, or a large polar amino acid"
; US-08-499-523-58

Query Match 69.2%; Score 63; DB 1; Length 18;
Best Local Similarity 66.7%; Pred. No. 0.0017;
Matches 12; Conservative 0; Mismatches 6; Indels 0; Gaps 0;

Qy 1 RGGRLSYRRRFFSTGSR 18
   ||||| |||||
Db 1 RGGRLCYRRRFFCVXGR 18

RESULT 18
US-09-128-345-53
; Sequence 53, Application US/09128345
; Patent No. 6159936
; GENERAL INFORMATION:
; APPLICANT: LEHRER, ROBERT I.
; APPLICANT: HARWIG, SYLVIA S.L.
; APPLICANT: KOKRYAKOV, VLADIMIR N.
; TITLE OF INVENTION: PROTEGRINS
; NUMBER OF SEQUENCES: 76
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: PENNIE & EDMONDS LLP
; STREET: 1155 Avenue of the Americas
; CITY: New York
; STATE: New York
; COUNTRY: USA
; ZIP: 10036-2711
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/128,345
; FILING DATE: 03-AUG-1998
; CLASSIFICATION: 514
; ATTORNEY/AGENT INFORMATION:
; NAME: Coruzzi, Laura, A.
; REGISTRATION NUMBER: 30,742
; REFERENCE/DOCKET NUMBER: 8067-0054-999
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (212) 790-9090
; TELEFAX: (212) 869-9741
; TELEX: 66141 PENNIE
; INFORMATION FOR SEQ ID NO: 53:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 18 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; FEATURE:
; NAME/KEY: Disulfide-bond
; LOCATION: 8..13

```

```
;
; NAME/KEY: Modified-site
; LOCATION: Group(6, 15)
; OTHER INFORMATION: /note= "X is a hydrophobic, a
; US-09-128-345-53
; OTHER INFORMATION: small, or a large polar amino acid"

Query Match 69.2%; Score 63; DB 2; Length 18;
Best Local Similarity 66.7%; Pred. No. 0.0017; 6; Indels 0; Gaps 0;
Matches 12; Conservative 0; Mismatches 6; Indels 0; Gaps 0;

QY 1 RGGRLSYRRRFFSTGTGR 18
    ||||| ||||| ||
Db 1 RGGRLXCRRRFFCVVGR 18

RESULT 19
US-09-128-345-58
; Sequence 58, Application US/09128345
; Patent No. 615936
; GENERAL INFORMATION:
; APPLICANT: LEHRER, ROBERT I.
; APPLICANT: HARWIG, SYLVIA S. L.
; APPLICANT: KOKRYAKOV, VLADIMIR N.
; TITLE OF INVENTION: PROTEGRINS
; NUMBER OF SEQUENCES: 76
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: PENNIE & EDMONDS LLP
; STREET: 1155 Avenue of the Americas
; CITY: New York
; STATE: New York
; COUNTRY: USA
; ZIP: 10036-2711
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/128,345
; FILING DATE: 03-AUG-1998
; CLASSIFICATION: 514
; ATTORNEY/AGENT INFORMATION:
; NAME: Cotuzzi, Laura, A.
; REGISTRATION NUMBER: 30,742
; REFERENCE/DOCKET NUMBER: 8067-0054-999
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (212) 790-9090
; TELEFAX: (212) 869-9741
; TELEX: 66141 PENNIE
; INFORMATION FOR SEQ ID NO: 58:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 18 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; FEATURE:
; NAME/KEY: Disulfide-bond
; LOCATION: 6..15
; FEATURE:
; NAME/KEY: Modified-site
; LOCATION: group(8, 13)
; OTHER INFORMATION: /note= "X is a hydrophobic, a
; US-09-128-345-58
; OTHER INFORMATION: small, or a large polar amino acid"

Query Match 69.2%; Score 63; DB 2; Length 18;
Best Local Similarity 66.7%; Pred. No. 0.0017; 6; Indels 0; Gaps 0;
Matches 12; Conservative 0; Mismatches 6; Indels 0; Gaps 0;

QY 1 RGGRLSYRRRFFSTGTGR 18
    ||||| ||||| ||
Db 1 RGGRLXCRRRFFCVVGR 18
```

```
RESULT 20
US-09-385-328-90
; Sequence 90, Application US/09385328
; Patent No. 6653442
; GENERAL INFORMATION:
; APPLICANT: Chang, Conway C.
; APPLICANT: Gu, Chee L.
; APPLICANT: Chen, Jie
; APPLICANT: Steinberg, Deborah A.
; APPLICANT: Lehrer, Robert I.
; APPLICANT: Harwig, Sylvia S. L.
; APPLICANT: Kokryakov, Vladimir N.
; TITLE OF INVENTION: PROTEGRINS
; FILE REFERENCE: 8067-0067-999
; CURRENT APPLICATION NUMBER: US/09/385,328
; CURRENT FILING DATE: 1999-08-30
; PRIOR APPLICATION NUMBER: US 09/128,345
; PRIOR FILING DATE: 1998-08-03
; PRIOR APPLICATION NUMBER: US 08/741,860
; PRIOR FILING DATE: 1996-10-28
; NUMBER OF SEQ ID NOS: 125
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 90
; LENGTH: 18
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Synthetic peptide
; NAME/KEY: AMIDATION
; LOCATION: 18
; OTHER INFORMATION: C-terminal amidation
; US-09-385-328-90

Query Match 69.2%; Score 63; DB 2; Length 18;
Best Local Similarity 66.7%; Pred. No. 0.0017; 4; Indels 0; Gaps 0;
Matches 12; Conservative 2; Mismatches 4; Indels 0; Gaps 0;

QY 1 RGGRLSYRRRFFSTGTGR 18
    ||||| ||||| ||
Db 1 RGGRLXCRRRFFCVVGR 18

RESULT 21
US-09-385-328-101
; Sequence 101, Application US/09385328
; Patent No. 6653442
; GENERAL INFORMATION:
; APPLICANT: Chang, Conway C.
; APPLICANT: Gu, Chee L.
; APPLICANT: Chen, Jie
; APPLICANT: Steinberg, Deborah A.
; APPLICANT: Lehrer, Robert I.
; APPLICANT: Harwig, Sylvia S. L.
; APPLICANT: Kokryakov, Vladimir N.
; TITLE OF INVENTION: PROTEGRINS
; FILE REFERENCE: 8067-0067-999
; CURRENT APPLICATION NUMBER: US/09/385,328
; CURRENT FILING DATE: 1999-08-30
; PRIOR APPLICATION NUMBER: US 09/128,345
; PRIOR FILING DATE: 1998-08-03
; PRIOR APPLICATION NUMBER: US 08/741,860
; PRIOR FILING DATE: 1996-10-28
; NUMBER OF SEQ ID NOS: 125
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 101
; LENGTH: 18
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Synthetic peptide
; NAME/KEY: AMIDATION
```



```
; LOCATION: 18
; OTHER INFORMATION: C-terminal amidation
; NAME/KEY: SITE
; LOCATION: 6, 15
; OTHER INFORMATION: Xaa = hydrophobic, small or large polar amino acid
; NAME/KEY: DISULFID
; LOCATION: (8)...(13)
US-09-385-328-101

Query Match          69.2%; Score 63; DB 2; Length 18;
Best Local Similarity 66.7%; Pred. No. 0.0017;
Matches 12; Conservative 0; Mismatches 6; Indels 0; Gaps 0;

Qy 1 RGGRLSYRRRPFSTGSR 18
    ||||| |||||
Db 1 RGGRLXYCRRRRCVXVGR 18

RESULT 22
US-09-385-328-106
; Sequence 106, Application US/09385328
; Patent No. 6653442
; GENERAL INFORMATION:
; APPLICANT: Chang, Conway C.
; APPLICANT: Gu, Chee L.
; APPLICANT: Chen, Jie
; APPLICANT: Steinberg, Deborah A.
; APPLICANT: Lehrer, Robert I.
; APPLICANT: Harwig, Sylvia S. L.
; APPLICANT: Kokryakov, Vladimir N.
; TITLE OF INVENTION: PROTEGRINS
; FILE REFERENCE: 8067-0067-999
; CURRENT APPLICATION NUMBER: US/09/385,328
; CURRENT FILING DATE: 1999-08-30
; PRIOR APPLICATION NUMBER: US 09/128,345
; PRIOR FILING DATE: 1998-08-03
; PRIOR APPLICATION NUMBER: US 08/741,860
; PRIOR FILING DATE: 1996-10-28
; NUMBER OF SEQ ID NOS: 125
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 106
; LENGTH: 18
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Synthetic peptide
; NAME/KEY: AMIDATION
; LOCATION: 18
; OTHER INFORMATION: C-terminal amidation
; NAME/KEY: SITE
; LOCATION: 8, 13
; OTHER INFORMATION: Xaa = hydrophobic, small or large polar amino acid
; NAME/KEY: DISULFID
; LOCATION: (6)...(15)
US-09-385-328-106

Query Match          69.2%; Score 63; DB 2; Length 18;
Best Local Similarity 66.7%; Pred. No. 0.0017;
Matches 12; Conservative 0; Mismatches 6; Indels 0; Gaps 0;

Qy 1 RGGRLSYRRRPFSTGSR 18
    ||||| |||||
Db 1 RGGRLCYRRRRCVXVGR 18

RESULT 23
US-08-499-523-54
; Sequence 54, Application US/08499523
; Patent No. 5804558
; GENERAL INFORMATION:
; APPLICANT: LEHRER, ROBERT I.
; APPLICANT: HARWIG, SYLVIA S.L.
; APPLICANT: KOKRYAKOV, VLADIMIR N.
; TITLE OF INVENTION: PROTEGRINS
; NUMBER OF SEQUENCES: 76
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: MORRISON & FOERSTER
; STREET: 2000 Pennsylvania Ave. N.W., Ste. 5500
; CITY: Washington
; STATE: DC
; COUNTRY: USA
; ZIP: 20006-1812
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
```

```
; TITLE OF INVENTION: PROTEGRINS
; NUMBER OF SEQUENCES: 76
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: MORRISON & FOERSTER
; STREET: 2000 Pennsylvania Ave. N.W., Ste. 5500
; CITY: Washington
; STATE: DC
; COUNTRY: USA
; ZIP: 20006-1812
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/499,523
; FILING DATE: 07-JUL-1995
; CLASSIFICATION: 514
; ATTORNEY/AGENT INFORMATION:
; NAME: MURASHIGE, KATE H.
; REGISTRATION NUMBER: 29,959
; REFERENCE/DOCKET NUMBER: 2000-0540.24
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (202) 887-1500
; TELEFAX: (202) 887-0763
; TELEX: 90-4030
; INFORMATION FOR SEQ ID NO: 54:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 18 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; FEATURE:
; NAME/KEY: Disulfide-bond
; LOCATION: 8..13
; NAME/KEY: Modified-site
; LOCATION: group(6, 15)
; OTHER INFORMATION: /note= "X is a hydrophobic, a
; OTHER INFORMATION: small, or a large polar amino acid"
US-08-499-523-54

Query Match          68.1%; Score 62; DB 1; Length 18;
Best Local Similarity 66.7%; Pred. No. 0.0024;
Matches 12; Conservative 0; Mismatches 6; Indels 0; Gaps 0;

Qy 1 RGGRLSYRRRPFSTGSR 18
    ||||| |||||
Db 1 RGGRLXYCRRRRCVXVGR 18

RESULT 24
US-08-499-523-59
; Sequence 59, Application US/08499523
; Patent No. 5804558
; GENERAL INFORMATION:
; APPLICANT: LEHRER, ROBERT I.
; APPLICANT: HARWIG, SYLVIA S.L.
; APPLICANT: KOKRYAKOV, VLADIMIR N.
; TITLE OF INVENTION: PROTEGRINS
; NUMBER OF SEQUENCES: 76
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: MORRISON & FOERSTER
; STREET: 2000 Pennsylvania Ave. N.W., Ste. 5500
; CITY: Washington
; STATE: DC
; COUNTRY: USA
; ZIP: 20006-1812
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
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; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/08/499,523  
; FILING DATE: 07-JUL-1995  
; CLASSIFICATION: 514  
; ATTORNEY/AGENT INFORMATION:  
; NAME: MURASHIGE, KATE H.  
; REGISTRATION NUMBER: 29,959  
; REFERENCE/DOCKET NUMBER: 2000-0540.24  
; TELEPHONE: (202) 887-1500  
; TELEFAX: (202) 887-0763  
; TELEX: 90-4030  
; INFORMATION FOR SEQ ID NO: 59:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 18 amino acids  
; TYPE: amino acid  
; STRANDEDNESS: single  
; TOPOLOGY: linear  
; FEATURE:  
; NAME/KEY: Disulfide-bond  
; LOCATION: 6..15  
; FEATURE:  
; NAME/KEY: Modified-site  
; LOCATION: group(8, 13)  
; OTHER INFORMATION: /note= "X is a hydrophobic, a  
; OTHER INFORMATION: small, or a large polar amino acid"  
US-08-499-523-59

Query Match 68.1%; Score 62; DB 1; Length 18;  
Best Local Similarity 66.7%; Pred. No. 0.0024;  
Matches 12; Conservative 0; Mismatches 6; Indels 0;

QY 1 RGRGLYSRRRSTSTGR 18  
|||||  
Db 1 RGRGLCYRRRFXICVGR 18

RESULT 25  
US-09-128-345-54  
; Sequence 54, Application US/09128345  
; Patent No. 6159936  
; GENERAL INFORMATION:  
; APPLICANT: LEHRER, ROBERT I.  
; APPLICANT: HARWIG, SYLVIA S.L.  
; APPLICANT: KORYAKOV, VLADIMIR N.  
; TITLE OF INVENTION: PROTEGRINS  
; NUMBER OF SEQUENCES: 76  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: PENNIE & EDMONDS LLP  
; STREET: 1155 Avenue of the Americas  
; CITY: New York  
; STATE: New York  
; COUNTRY: USA  
; ZIP: 10036-2711  
; COMPUTER READABLE FORM:  
; COMPUTER: IBM PC compatible  
; OPERATING SYSTEM: PC-DOS/MS-DOS  
; SOFTWARE: Patent In Release #1.0, Version #1.30  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/09/128,345  
; FILING DATE: 03-AUG-1998  
; CLASSIFICATION: 514  
; ATTORNEY/AGENT INFORMATION:  
; NAME: Coruzzi, Laura, A.  
; REGISTRATION NUMBER: 30,742  
; REFERENCE/DOCKET NUMBER: 8067-0054-999  
; TELEPHONE: (212) 790-9090  
; TELEFAX: (212) 869-9741  
; INFORMATION FOR SEQ ID NO: 54:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 18 amino acids  
; TYPE: amino acid  
; STRANDEDNESS: single  
; TOPOLOGY: linear  
; FEATURE:  
; NAME/KEY: Disulfide-bond  
; LOCATION: 6..15  
; FEATURE:  
; NAME/KEY: Modified-site  
; LOCATION: group(8, 13)  
; OTHER INFORMATION: /note= "X is a hydrophobic, a  
; OTHER INFORMATION: small, or a large polar amino acid"  
US-09-128-345-59

; LENGTH: 18 amino acids  
; TYPE: amino acid  
; STRANDEDNESS: single  
; TOPOLOGY: linear  
; FEATURE:  
; NAME/KEY: Disulfide-bond  
; LOCATION: 8..13  
; FEATURE:  
; NAME/KEY: Modified-site  
; LOCATION: group(6, 15)  
; OTHER INFORMATION: /note= "X is a hydrophobic, a  
; OTHER INFORMATION: small, or a large polar amino acid"  
US-09-128-345-54

Query Match 68.1%; Score 62; DB 2; Length 18;  
Best Local Similarity 66.7%; Pred. No. 0.0024;  
Matches 12; Conservative 0; Mismatches 6; Indels 0; Gaps 0;

QY 1 RGRGLYSRRRSTSTGR 18  
|||||  
Db 1 RGRGLCYRRRFXICVGR 18

RESULT 26  
US-09-128-345-59  
; Sequence 59, Application US/09128345  
; Patent No. 6159936  
; GENERAL INFORMATION:  
; APPLICANT: LEHRER, ROBERT I.  
; APPLICANT: HARWIG, SYLVIA S.L.  
; APPLICANT: KORYAKOV, VLADIMIR N.  
; TITLE OF INVENTION: PROTEGRINS  
; NUMBER OF SEQUENCES: 76  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: PENNIE & EDMONDS LLP  
; STREET: 1155 Avenue of the Americas  
; CITY: New York  
; STATE: New York  
; COUNTRY: USA  
; ZIP: 10036-2711  
; COMPUTER READABLE FORM:  
; COMPUTER: IBM PC compatible  
; OPERATING SYSTEM: PC-DOS/MS-DOS  
; SOFTWARE: Patent In Release #1.0, Version #1.30  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/09/128,345  
; FILING DATE: 03-AUG-1998  
; CLASSIFICATION: 514  
; ATTORNEY/AGENT INFORMATION:  
; NAME: Coruzzi, Laura, A.  
; REGISTRATION NUMBER: 30,742  
; REFERENCE/DOCKET NUMBER: 8067-0054-999  
; TELEPHONE: (212) 790-9090  
; TELEFAX: (212) 869-9741  
; INFORMATION FOR SEQ ID NO: 59:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 18 amino acids  
; TYPE: amino acid  
; STRANDEDNESS: single  
; TOPOLOGY: linear  
; FEATURE:  
; NAME/KEY: Disulfide-bond  
; LOCATION: 6..15  
; FEATURE:  
; NAME/KEY: Modified-site  
; LOCATION: group(8, 13)  
; OTHER INFORMATION: /note= "X is a hydrophobic, a  
; OTHER INFORMATION: small, or a large polar amino acid"  
US-09-128-345-59

Query Match 68.1%; Score 62; DB 2; Length 18;  
Best Local Similarity 66.7%; Pred. No. 0.0024;  
Matches 12; Conservative 0; Mismatches 6; Indels 0; Gaps 0;

QY 1 RGGRLSYRRRPFSTGTGR 18  
||||| |||||  
Db 1 RGGRLCYRRRPFICVGR 18

## RESULT 27

US-09-385-328-102  
; Sequence 102, Application US/09385328  
; Patent No. 6653442  
; GENERAL INFORMATION:  
; APPLICANT: Chang, Conway C.  
; APPLICANT: Gu, Chee L.  
; APPLICANT: Chen, Jie  
; APPLICANT: Steinberg, Deborah A.  
; APPLICANT: Lehrer, Robert I.  
; APPLICANT: Harwig, Sylvia S. L.  
; APPLICANT: Kokryakov, Vladimir N.  
; TITLE OF INVENTION: PROTEGRINS  
; FILE REFERENCE: 8067-0067-999  
; CURRENT APPLICATION NUMBER: US/09/385,328  
; CURRENT FILING DATE: 1999-08-30  
; PRIOR APPLICATION NUMBER: US 09/128,345  
; PRIOR FILING DATE: 1998-08-03  
; PRIOR APPLICATION NUMBER: US 08/741,860  
; PRIOR FILING DATE: 1996-10-28  
; NUMBER OF SEQ ID NOS: 125  
; SOFTWARE: FastSeq for Windows Version 4.0  
; SEQ ID NO 102  
; LENGTH: 18  
; TYPE: PRT  
; ORGANISM: Artificial Sequence  
; FEATURE:  
; OTHER INFORMATION: Synthetic peptide  
; NAME/KEY: AMIDATION  
; LOCATION: 18  
; OTHER INFORMATION: C-terminal amidation  
; NAME/KEY: SITE  
; LOCATION: 6, 15  
; OTHER INFORMATION: Xaa = hydrophobic, small or large polar amino acid  
; NAME/KEY: DISULFID  
; LOCATION: (8)...(13)  
US-09-385-328-102

Query Match 68.1%; Score 62; DB 2; Length 18;  
Best Local Similarity 66.7%; Pred. No. 0.0024;  
Matches 12; Conservative 0; Mismatches 6; Indels 0; Gaps 0;

QY 1 RGGRLSYRRRPFSTGTGR 18  
||||| |||||  
Db 1 RGGRLCYRRRPFICVGR 18

## RESULT 28

US-09-385-328-107  
; Sequence 107, Application US/09385328  
; Patent No. 6653442  
; GENERAL INFORMATION:  
; APPLICANT: Chang, Conway C.  
; APPLICANT: Gu, Chee L.  
; APPLICANT: Chen, Jie  
; APPLICANT: Steinberg, Deborah A.  
; APPLICANT: Lehrer, Robert I.  
; APPLICANT: Harwig, Sylvia S. L.  
; APPLICANT: Kokryakov, Vladimir N.  
; TITLE OF INVENTION: PROTEGRINS  
; FILE REFERENCE: 8067-0067-999  
; CURRENT APPLICATION NUMBER: US/09/385,328  
; CURRENT FILING DATE: 1999-08-30  
; PRIOR APPLICATION NUMBER: US 09/128,345

; PRIOR FILING DATE: 1998-08-03  
; PRIOR APPLICATION NUMBER: US 08/741,860  
; PRIOR FILING DATE: 1996-10-28  
; NUMBER OF SEQ ID NOS: 125  
; SOFTWARE: FastSeq for Windows Version 4.0  
; SEQ ID NO 107  
; LENGTH: 18  
; TYPE: PRT  
; ORGANISM: Artificial Sequence  
; FEATURE:  
; OTHER INFORMATION: Synthetic peptide  
; NAME/KEY: AMIDATION  
; LOCATION: 18  
; OTHER INFORMATION: C-terminal amidation  
; NAME/KEY: SITE  
; LOCATION: 8, 13  
; OTHER INFORMATION: Xaa = hydrophobic, small or large polar amino acid  
; NAME/KEY: DISULFID  
; LOCATION: (6)...(15)  
US-09-385-328-107

Query Match 68.1%; Score 62; DB 2; Length 18;  
Best Local Similarity 66.7%; Pred. No. 0.0024;  
Matches 12; Conservative 0; Mismatches 6; Indels 0; Gaps 0;

QY 1 RGGRLSYRRRPFSTGTGR 18  
||||| |||||  
Db 1 RGGRLCYRRRPFICVGR 18

## RESULT 29

US-08-095-769A-1  
; Sequence 1, Application US/08095769A  
; Patent No. 5464823  
; GENERAL INFORMATION:  
; APPLICANT: LEHRER, ROBERT I.  
; APPLICANT: KOKRYAKOV, VLADIMIR N.  
; APPLICANT: HARWIG, SYLVIA S. L.  
; TITLE OF INVENTION: NOVEL MAMMALIAN ANTIBIOTIC PEPTIDES  
; NUMBER OF SEQUENCES: 5  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: MORRISON & FOERSTER  
; STREET: 2000 Pennsylvania Ave. N.W., Ste. 5500  
; CITY: Washington, DC  
; COUNTRY: USA  
; ZIP: 20006-1812  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Floppy disk  
; COMPUTER: IBM PC compatible  
; OPERATING SYSTEM: PC-DOS/MS-DOS  
; SOFTWARE: Patent In Release #1.0, Version #1.25  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/08/095,769A  
; FILING DATE: 26-JUL-1993  
; CLASSIFICATION: 435  
; ATTORNEY/AGENT INFORMATION:  
; NAME: MURASHIGE, KATE H.  
; REGISTRATION NUMBER: 29,959  
; REFERENCE/DOCKET NUMBER: 220002054020  
; TELEPHONE: (202) 887-1500  
; TELEFAX: (202) 887-0763  
; TELEX: 90-4030  
; INFORMATION FOR SEQ ID NO: 1:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 18 amino acids  
; TYPE: amino acid  
; STRANDEDNESS: single  
; TOPOLOGY: linear  
US-08-095-769A-1

Query Match 67.0%; Score 61; DB 1; Length 18;  
Best Local Similarity 66.7%; Pred. No. 0.0035;

```
Matches 12; Conservative 0; Mismatches 6; Indels 0; Gaps 0;

Qy 1 RGRGLYSRRRSTSTGR 18
    ||||| ||||| ||
Db 1 RGRGLCYCRRRRCVCVGR 18

RESULT 30
US-08-182-483A-2
; Sequence 2, Application US/08182483A
; Patent No. 5693486
; GENERAL INFORMATION:
; APPLICANT: LEHRER, ROBERT I.
; APPLICANT: KOKRYAKOV, VLADIMIR N.
; APPLICANT: HARWIG, SYLVIA S.L.
; TITLE OF INVENTION: NOVEL ANTIBIOTIC PEPTIDES
; NUMBER OF SEQUENCES: 31
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: MORRISON & FOERSTER
; STREET: 2000 Pennsylvania Ave. N.W., Ste. 5500
; CITY: Washington
; STATE: DC
; COUNTRY: USA
; ZIP: 20006-1812
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/182,483A
; FILING DATE: 13-JAN-1994
; CLASSIFICATION: 435
; ATTORNEY/AGENT INFORMATION:
; NAME: MURASHIGE, KATE H.
; REGISTRATION/DOCKET NUMBER: 29,959
; REFERENCE/DOCKET NUMBER: 2000-0540.21
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (202) 887-1500
; TELEFAX: (202) 887-0763
; TELEX: 90-4030
; INFORMATION FOR SEQ ID NO: 2:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 18 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
US-08-182-483A-2

Query Match 67.0%; Score 61; DB 1; Length 18;
Best Local Similarity 66.7%; Pred. No. 0.0035;
Matches 12; Conservative 0; Mismatches 6; Indels 0; Gaps 0;

Qy 1 RGRGLYSRRRSTSTGR 18
    ||||| ||||| ||
Db 1 RGRGLCYCRRRRCVCVGR 18

RESULT 31
US-08-182-483A-28
; Sequence 28, Application US/08182483A
; Patent No. 5693486
; GENERAL INFORMATION:
; APPLICANT: LEHRER, ROBERT I.
; APPLICANT: KOKRYAKOV, VLADIMIR N.
; APPLICANT: HARWIG, SYLVIA S.L.
; TITLE OF INVENTION: NOVEL ANTIBIOTIC PEPTIDES
; NUMBER OF SEQUENCES: 31
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: MORRISON & FOERSTER
; STREET: 2000 Pennsylvania Ave. N.W., Ste. 5500
; CITY: Washington
; STATE: DC
; COUNTRY: USA
; ZIP: 20006-1812
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/243,879A
; FILING DATE: 17-MAY-1994
; CLASSIFICATION: 530
; ATTORNEY/AGENT INFORMATION:
; NAME: MURASHIGE, KATE H.
; REGISTRATION/DOCKET NUMBER: 29,959
; REFERENCE/DOCKET NUMBER: 2000-0540.22
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (202) 887-1500
; TELEFAX: (202) 887-0763
; TELEX: 90-4030
; INFORMATION FOR SEQ ID NO: 1:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 18 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
```

```
; COUNTRY: USA
; ZIP: 20006-1812
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/182,483A
; FILING DATE: 13-JAN-1994
; CLASSIFICATION: 435
; ATTORNEY/AGENT INFORMATION:
; NAME: MURASHIGE, KATE H.
; REGISTRATION/DOCKET NUMBER: 29,959
; REFERENCE/DOCKET NUMBER: 2000-0540.21
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (202) 887-1500
; TELEFAX: (202) 887-0763
; TELEX: 90-4030
; INFORMATION FOR SEQ ID NO: 28:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 18 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
US-08-182-483A-28

Query Match 67.0%; Score 61; DB 1; Length 18;
Best Local Similarity 66.7%; Pred. No. 0.0035;
Matches 12; Conservative 2; Mismatches 4; Indels 0; Gaps 0;

Qy 1 RGRGLYSRRRSTSTGR 18
    ||||| ||||| ||
Db 1 RGRGLCYCRRRRCVCVGR 18

RESULT 32
US-08-243-879A-1
; Sequence 1, Application US/08243879A
; Patent No. 5708145
; GENERAL INFORMATION:
; APPLICANT: LEHRER, ROBERT I.
; APPLICANT: HARWIG, SYLVIA S.L.
; TITLE OF INVENTION: A NEW PROTEGRIN
; NUMBER OF SEQUENCES: 42
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: MORRISON & FOERSTER
; STREET: 2000 Pennsylvania Ave. N.W., Ste. 5500
; CITY: Washington, DC
; COUNTRY: USA
; ZIP: 20006-1812
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/243,879A
; FILING DATE: 17-MAY-1994
; CLASSIFICATION: 530
; ATTORNEY/AGENT INFORMATION:
; NAME: MURASHIGE, KATE H.
; REGISTRATION/DOCKET NUMBER: 29,959
; REFERENCE/DOCKET NUMBER: 2000-0540.22
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (202) 887-1500
; TELEFAX: (202) 887-0763
; TELEX: 90-4030
; INFORMATION FOR SEQ ID NO: 1:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 18 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
```

```
; TOPOLOGY: linear
US-08-243-879A-1
Query Match 67.0%; Score 61; DB 1; Length 18;
Best Local Similarity 66.7%; Pred. No. 0.0035;
Matches 12; Conservative 0; Mismatches 6; Indels 0; Gaps 0;

Qy 1 RGGRLSYRRRPFSTGTGR 18
    ||||| ||||| ||
Db 1 RGGRLCYRRRRFCVCVGR 18
    ||||| ||||| ||

RESULT 33
US-08-243-879A-27
; Sequence 27, Application US/08243879A
; Patent No. 5708145
; GENERAL INFORMATION:
; APPLICANT: LEHRER, ROBERT I.
; APPLICANT: HARWIG, SYLVIA S.L.
; TITLE OF INVENTION: A NEW PROTEGRIN
; NUMBER OF SEQUENCES: 42
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: MORRISON & FOERSTER
; STREET: 2000 Pennsylvania Ave. N.W., Ste. 5500
; CITY: Washington, DC
; COUNTRY: USA
; ZIP: 20006-1812
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patentin Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/243.879A
; FILING DATE: 17-MAY-1994
; CLASSIFICATION: 530
; ATTORNEY/AGENT INFORMATION:
; NAME: MURASHIGE, KATE H.
; REGISTRATION NUMBER: 29,959
; REFERENCE/DOCKET NUMBER: 2000-0540.22
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (202) 887-1500
; TELEFAX: (202) 887-0763
; TELEX: 90-4030
; INFORMATION FOR SEQ ID NO: 27:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 18 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
US-08-243-879A-27

Query Match 67.0%; Score 61; DB 1; Length 18;
Best Local Similarity 66.7%; Pred. No. 0.0035;
Matches 12; Conservative 2; Mismatches 4; Indels 0; Gaps 0;

Qy 1 RGGRLSYRRRPFSTGTGR 18
    ||||| ||||| ||
Db 1 RATFISFRRRPFVSVCGR 18
    ||||| ||||| ||

RESULT 34
US-08-499-523-11
; Sequence 11, Application US/08499523
; Patent No. 5804558
; GENERAL INFORMATION:
; APPLICANT: LEHRER, ROBERT I.
; APPLICANT: HARWIG, SYLVIA S.L.
; APPLICANT: KORYAKOV, VLADIMIR N.
; TITLE OF INVENTION: PROTEGRINS
; NUMBER OF SEQUENCES: 76
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: MORRISON & FOERSTER
; STREET: 2000 Pennsylvania Ave. N.W., Ste. 5500
; CITY: Washington
; STATE: DC
; COUNTRY: USA
; ZIP: 20006-1812
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patentin Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/499,523
; FILING DATE: 07-JUL-1995
; CLASSIFICATION: 514
; ATTORNEY/AGENT INFORMATION:
; NAME: MURASHIGE, KATE H.
```

```
; STREET: 2000 Pennsylvania Ave. N.W., Ste. 5500
; CITY: Washington
; STATE: DC
; COUNTRY: USA
; ZIP: 20006-1812
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patentin Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/499,523
; FILING DATE: 07-JUL-1995
; CLASSIFICATION: 514
; ATTORNEY/AGENT INFORMATION:
; NAME: MURASHIGE, KATE H.
; REGISTRATION NUMBER: 29,959
; REFERENCE/DOCKET NUMBER: 2000-0540.24
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (202) 887-1500
; TELEFAX: (202) 887-0763
; TELEX: 90-4030
; INFORMATION FOR SEQ ID NO: 11:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 18 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; FEATURE:
; NAME/KEY: Disulfide-bond
; LOCATION: 4..13
; FEATURE:
; NAME/KEY: Disulfide-bond
; LOCATION: 6..11
US-08-499-523-11

Query Match 67.0%; Score 61; DB 1; Length 18;
Best Local Similarity 66.7%; Pred. No. 0.0035;
Matches 12; Conservative 0; Mismatches 6; Indels 0; Gaps 0;

Qy 1 RGGRLSYRRRPFSTGTGR 18
    ||||| ||||| ||
Db 1 RGGRLCYRRRRFCVCVGR 18
    ||||| ||||| ||

RESULT 35
US-08-499-523-16
; Sequence 16, Application US/08499523
; Patent No. 5804558
; GENERAL INFORMATION:
; APPLICANT: LEHRER, ROBERT I.
; APPLICANT: HARWIG, SYLVIA S.L.
; APPLICANT: KORYAKOV, VLADIMIR N.
; TITLE OF INVENTION: PROTEGRINS
; NUMBER OF SEQUENCES: 76
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: MORRISON & FOERSTER
; STREET: 2000 Pennsylvania Ave. N.W., Ste. 5500
; CITY: Washington
; STATE: DC
; COUNTRY: USA
; ZIP: 20006-1812
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patentin Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/499,523
; FILING DATE: 07-JUL-1995
; CLASSIFICATION: 514
; ATTORNEY/AGENT INFORMATION:
; NAME: MURASHIGE, KATE H.
```

REGISTRATION NUMBER: 29,959  
REFERENCE/DOCKET NUMBER: 2000-0540.24  
TELEPHONE: (202) 887-1500  
TELEFAX: (202) 887-0763  
TELEX: 90-4030  
INFORMATION FOR SEQ ID NO: 16:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 18 amino acids  
TYPE: amino acid  
STRANDEDNESS: single  
TOPOLOGY: linear  
US-08-499-523-16

Query Match 67.0%; Score 61; DB 1; Length 18;  
Best Local Similarity 66.7%; Pred. No. 0.0035;  
Matches 12; Conservative 0; Mismatches 6; Indels 0; Gaps 0;

QY 1 RGRRLSYRRRSTSTGR 18  
||||| | | | | |  
DB 1 RGRRLCYCRRRCVCVGR 18

RESULT 36  
US-08-499-523-33  
Sequence 33, Application US/08499523  
Patent No. 5804558  
GENERAL INFORMATION:  
APPLICANT: LEHRER, ROBERT I.  
APPLICANT: HARWIG, SYLVIA S.L.  
APPLICANT: KOKRYAKOV, VLADIMIR N.  
TITLE OF INVENTION: PROTEGRINS  
NUMBER OF SEQUENCES: 76  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: MORRISON & FOERSTER  
STREET: 2000 Pennsylvania Ave. N.W., Ste. 5500  
CITY: Washington  
STATE: DC  
COUNTRY: USA  
ZIP: 20006-1812

COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: PatentIn Release #1.0, Version #1.30  
CURRENT APPLICATION DATA:  
FILING DATE: 07-JUL-1995  
CLASSIFICATION: 514  
ATTORNEY/AGENT INFORMATION:  
NAME: MURASHIGE, KATE H.  
REGISTRATION NUMBER: 29,959  
REFERENCE/DOCKET NUMBER: 2000-0540.24  
TELEPHONE: (202) 887-1500  
TELEFAX: (202) 887-0763  
TELEX: 90-4030

INFORMATION FOR SEQ ID NO: 33:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 18 amino acids  
TYPE: amino acid  
STRANDEDNESS: single  
TOPOLOGY: linear  
FEATURE:  
NAME/KEY: Region  
LOCATION: 1..18  
OTHER INFORMATION: /note= "All D-form amino acids"

US-08-499-523-33  
Query Match 67.0%; Score 61; DB 1; Length 18;  
Best Local Similarity 66.7%; Pred. No. 0.0035;  
Matches 12; Conservative 0; Mismatches 6; Indels 0; Gaps 0;

QY 1 RGRRLSYRRRSTSTGR 18  
||||| | | | | |  
DB 1 RGRRLCYCRRRCVCVGR 18

RESULT 37  
US-08-499-523-48  
Sequence 48, Application US/08499523  
Patent No. 5804558  
GENERAL INFORMATION:  
APPLICANT: LEHRER, ROBERT I.  
APPLICANT: HARWIG, SYLVIA S.L.  
APPLICANT: KOKRYAKOV, VLADIMIR N.  
TITLE OF INVENTION: PROTEGRINS  
NUMBER OF SEQUENCES: 76  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: MORRISON & FOERSTER  
STREET: 2000 Pennsylvania Ave. N.W., Ste. 5500  
CITY: Washington  
STATE: DC  
COUNTRY: USA  
ZIP: 20006-1812

COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: PatentIn Release #1.0, Version #1.30  
CURRENT APPLICATION DATA:  
FILING DATE: 07-JUL-1995  
CLASSIFICATION: 514  
ATTORNEY/AGENT INFORMATION:  
NAME: MURASHIGE, KATE H.  
REGISTRATION NUMBER: 29,959  
REFERENCE/DOCKET NUMBER: 2000-0540.24  
TELEPHONE: (202) 887-1500  
TELEFAX: (202) 887-0763  
TELEX: 90-4030

INFORMATION FOR SEQ ID NO: 48:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 18 amino acids  
TYPE: amino acid  
STRANDEDNESS: single  
TOPOLOGY: linear  
US-08-499-523-48

Query Match 67.0%; Score 61; DB 1; Length 18;  
Best Local Similarity 66.7%; Pred. No. 0.0035;  
Matches 12; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

QY 1 RGRRLSYRRRSTSTGR 18  
||||| | | | | |  
DB 1 RGRRLCYCRRRCVCVGR 18

RESULT 38  
US-08-752-852A-1  
Sequence 1, Application US/08752852A  
Patent No. 5994306  
GENERAL INFORMATION:  
APPLICANT: Chang, Conway  
APPLICANT: Gu, Chee-Liang  
APPLICANT: Chen, Jie  
APPLICANT: Steinberg, Deborah  
APPLICANT: Lehrer, Robert  
APPLICANT: Harwig, Sylvia  
TITLE OF INVENTION: FINE-TUNED PROTEGRINS  
NUMBER OF SEQUENCES: 242  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: PENNIE & EDMONDS LLP  
STREET: 1155 Avenue of the Americas  
CITY: New York

US-08-752-852A-1  
Query Match 67.0%; Score 61; DB 1; Length 18;  
Best Local Similarity 66.7%; Pred. No. 0.0035;  
Matches 12; Conservative 0; Mismatches 6; Indels 0; Gaps 0;

STATE: NY  
COUNTRY: USA  
ZIP: 10036-2711  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Diskette  
COMPUTER: IBM Compatible  
OPERATING SYSTEM: DOS  
SOFTWARE: FastSeq Version 2.0  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/752,852A  
FILING DATE: 21-NOV-1996  
CLASSIFICATION: 435  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER:  
FILING DATE:  
ATTORNEY/AGENT INFORMATION:  
NAME: Coruzzi, Laura A.  
REGISTRATION NUMBER: 30,742  
REFERENCE/DOCKET NUMBER: 8067-034-999  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: 212-790-9090  
TELEFAX: 212-869-9741  
TELEX: 66141  
INFORMATION FOR SEQ ID NO: 1:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 18 amino acids  
TYPE: amino acid  
STRANDEDNESS: unknown  
TOPOLOGY: unknown  
MOLECULE TYPE: peptide  
US-08-752-852A-1

Query Match 67.0%; Score 61; DB 1; Length 18;  
Best Local Similarity 66.7%; Pred. No. 0.0035;  
Matches 12; Conservative 0; Mismatches 6; Indels 0; Gaps 0;

QY 1 RGGRLSYRRRFFSTGTGR 18  
||||| ||||| ||  
Db 1 RGGRLCYRRRFFCVCVGR 18

RESULT 39  
US-08-752-852A-9  
Sequence 9, Application US/08752852A  
Patent No. 5994306  
GENERAL INFORMATION:  
APPLICANT: Chang, Conway  
APPLICANT: Gu, Chee-Liang  
APPLICANT: Chen, Jie  
APPLICANT: Steinberg, Deborah  
APPLICANT: Lehrner, Robert  
APPLICANT: Harwig, Sylvia  
TITLE OF INVENTION: FINE-TUNED PROTEGRINS  
NUMBER OF SEQUENCES: 242  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: PENNIE & EDMONDS LLP  
STREET: 1155 Avenue of the Americas  
CITY: New York  
STATE: NY  
COUNTRY: USA  
ZIP: 10036-2711  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Diskette  
COMPUTER: IBM Compatible  
OPERATING SYSTEM: DOS  
SOFTWARE: FastSeq Version 2.0  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/752,852A  
FILING DATE: 21-NOV-1996  
CLASSIFICATION: 435  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER:  
FILING DATE:

ATTORNEY/AGENT INFORMATION:  
NAME: Coruzzi, Laura A.  
REGISTRATION NUMBER: 30,742  
REFERENCE/DOCKET NUMBER: 8067-034-999  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: 212-790-9090  
TELEFAX: 212-869-9741  
TELEX: 66141  
INFORMATION FOR SEQ ID NO: 9:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 18 amino acids  
TYPE: amino acid  
STRANDEDNESS: unknown  
TOPOLOGY: unknown  
MOLECULE TYPE: peptide  
FEATURE:  
NAME/KEY: Other  
LOCATION: 14...15  
OTHER INFORMATION: Xaa=N-methyl valine  
US-08-752-852A-9

Query Match 67.0%; Score 61; DB 1; Length 18;  
Best Local Similarity 66.7%; Pred. No. 0.0035;  
Matches 12; Conservative 0; Mismatches 6; Indels 0; Gaps 0;

QY 1 RGGRLSYRRRFFSTGTGR 18  
||||| ||||| ||  
Db 1 RGGRLCYRRRFFCVCVGR 18

RESULT 40  
US-08-752-852A-123  
Sequence 123, Application US/08752852A  
Patent No. 5994306  
GENERAL INFORMATION:  
APPLICANT: Chang, Conway  
APPLICANT: Gu, Chee-Liang  
APPLICANT: Chen, Jie  
APPLICANT: Steinberg, Deborah  
APPLICANT: Lehrner, Robert  
APPLICANT: Harwig, Sylvia  
TITLE OF INVENTION: FINE-TUNED PROTEGRINS  
NUMBER OF SEQUENCES: 242  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: PENNIE & EDMONDS LLP  
STREET: 1155 Avenue of the Americas  
CITY: New York  
STATE: NY  
COUNTRY: USA  
ZIP: 10036-2711  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Diskette  
COMPUTER: IBM Compatible  
OPERATING SYSTEM: DOS  
SOFTWARE: FastSeq Version 2.0  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/752,852A  
FILING DATE: 21-NOV-1996  
CLASSIFICATION: 435  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER:  
FILING DATE:  
ATTORNEY/AGENT INFORMATION:  
NAME: Coruzzi, Laura A.  
REGISTRATION NUMBER: 30,742  
REFERENCE/DOCKET NUMBER: 8067-034-999  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: 212-790-9090  
TELEFAX: 212-869-9741  
TELEX: 66141  
INFORMATION FOR SEQ ID NO: 123:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 18 amino acids

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; TYPE: amino acid
; STRANDEDNESS: unknown
; TOPOLOGY: unknown
; MOLECULE TYPE: peptide
US-08-752-852A-123
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Query Match      67.0%; Score 61; DB 1; Length 18;
Best Local Similarity 66.7%; Pred. No. 0.0035;
Matches 12; Conservative 0; Mismatches 6; Indels 0; Gaps 0;
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QY      1 RGRGLSYRRRPFSTSTGR 18
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Db       1 RGRGLCYRRRPFSTSTGR 18
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Search completed: May 21, 2006, 00:25:42
Job time : 52 secs
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GenCore version 5.1.8  
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OM protein - protein search, using sw model

Run on: May 21, 2006, 00:36:11 ; Search time 181 Seconds  
(without alignments)  
46.066 Million cell updates/sec

Title: US-09-857-000a-11

Perfect score: 91

Sequence: 1 RGGLSYSRRRPFSTSTGR 18

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 2097797 seqs, 463214858 residues

Total number of hits satisfying chosen parameters: 2097797

Minimum DB seq length: 0

Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 100 summaries

Database : Published Applications AA Main.\*

1: /EMC\_Celerra\_SIDS3/ptodata/2/pubpaa/US07\_PUBCOMB.pep.\*  
2: /EMC\_Celerra\_SIDS3/ptodata/2/pubpaa/US08\_PUBCOMB.pep.\*  
3: /EMC\_Celerra\_SIDS3/ptodata/2/pubpaa/US09\_PUBCOMB.pep.\*  
4: /EMC\_Celerra\_SIDS3/ptodata/2/pubpaa/US10A\_PUBCOMB.pep.\*  
5: /EMC\_Celerra\_SIDS3/ptodata/2/pubpaa/US10B\_PUBCOMB.pep.\*  
6: /EMC\_Celerra\_SIDS3/ptodata/2/pubpaa/US11\_PUBCOMB.pep.\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

## SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	91	100.0	18	4	US-10-336-312-1
2	91	100.0	18	4	US-10-136-187-24
3	91	100.0	18	4	US-10-144-549-17
4	91	100.0	18	4	US-10-185-593-3
5	91	100.0	18	4	US-10-270-010-10
6	91	100.0	18	5	US-10-850-873-24
7	91	100.0	18	5	US-10-878-175B-36
8	91	100.0	18	5	US-10-923-112A-36
9	91	100.0	18	6	US-11-027-967-3
10	81	89.0	18	4	US-10-270-010-7
11	80	87.9	16	5	US-10-500-671A-15
12	80	87.9	18	3	US-09-810-601-42
13	79	86.8	18	4	US-10-336-312-26
14	73	80.2	18	4	US-10-336-312-27
15	73	80.2	18	6	US-11-016-318-2
16	69	75.8	18	4	US-10-336-312-7
17	65	71.4	18	3	US-09-539-443-63
18	65	71.4	18	3	US-09-539-443-67
19	65	71.4	18	4	US-10-627-829-63
20	65	71.4	18	4	US-10-627-829-67
21	63	69.2	18	3	US-09-539-443-53
22	63	69.2	18	3	US-09-539-443-58
23	63	69.2	18	4	US-10-627-829-53
24	63	69.2	18	4	US-10-627-829-58
25	62	68.1	18	3	US-09-539-443-54
26	62	68.1	18	3	US-09-539-443-59
27	62	68.1	18	4	US-10-627-829-54

28	62	68.1	18	4	US-10-627-829-59
29	61	67.0	18	3	US-09-030-619-221
30	61	67.0	18	3	US-09-912-609-109
31	61	67.0	18	3	US-09-539-443-11
32	61	67.0	18	3	US-09-539-443-16
33	61	67.0	18	3	US-09-539-443-33
34	61	67.0	18	3	US-09-539-443-48
35	61	67.0	18	4	US-10-077-624-15
36	61	67.0	18	4	US-10-313-994-11
37	61	67.0	18	4	US-10-277-232-221
38	61	67.0	18	4	US-10-277-233-221
39	61	67.0	18	4	US-10-427-715-32
40	61	67.0	18	4	US-10-427-715-33
41	61	67.0	18	4	US-10-706-391-15
42	61	67.0	18	4	US-10-627-829-11
43	61	67.0	18	4	US-10-627-829-16
44	61	67.0	18	4	US-10-627-829-33
45	61	67.0	18	4	US-10-627-829-48
46	61	67.0	18	5	US-10-838-289-745
47	61	67.0	18	6	US-11-066-697-1019
48	61	67.0	18	6	US-11-068-783-102
49	61	67.0	18	6	US-11-126-468-11
50	61	67.0	19	3	US-09-917-340-17
51	61	67.0	19	5	US-10-844-837-17
52	61	67.0	19	5	US-10-909-119-32
53	61	67.0	19	5	US-10-657-851-17
54	61	67.0	149	3	US-09-539-443-2
55	61	67.0	149	3	US-09-539-443-10
56	61	67.0	149	4	US-10-627-829-2
57	61	67.0	149	4	US-10-627-829-10
58	60	65.9	18	3	US-09-539-443-37
59	60	65.9	18	3	US-09-539-443-45
60	60	65.9	18	4	US-10-336-312-46
61	60	65.9	18	4	US-10-627-829-37
62	60	65.9	18	4	US-10-627-829-45
63	59	64.8	18	3	US-09-865-943-90
64	58	63.7	18	3	US-09-539-443-65
65	58	63.7	18	4	US-10-336-312-4
66	58	63.7	18	4	US-10-627-829-65
67	57	62.6	18	3	US-09-865-943-60
68	57	62.6	18	3	US-09-865-943-185
69	57	62.6	18	4	US-10-336-312-8
70	56	61.5	18	3	US-09-539-443-46
71	56	61.5	18	3	US-09-539-443-55
72	56	61.5	18	3	US-09-539-443-57
73	56	61.5	18	3	US-09-539-443-60
74	56	61.5	18	3	US-09-539-443-62
75	56	61.5	18	4	US-10-336-312-9
76	56	61.5	18	4	US-10-427-715-34
77	56	61.5	18	4	US-10-427-715-35
78	56	61.5	18	4	US-10-427-715-36
79	56	61.5	18	4	US-10-627-829-46
80	56	61.5	18	4	US-10-627-829-55
81	56	61.5	18	4	US-10-627-829-57
82	56	61.5	18	4	US-10-627-829-60
83	56	61.5	18	4	US-10-627-829-62
84	55	60.4	17	4	US-10-344-709C-19
85	55	60.4	18	3	US-09-865-943-69
86	55	60.4	18	3	US-09-865-943-88
87	55	60.4	18	3	US-09-865-943-191
88	55	60.4	18	3	US-09-539-443-39
89	55	60.4	18	3	US-09-539-443-49
90	55	60.4	18	4	US-10-627-829-39
91	55	60.4	18	4	US-10-627-829-49
92	55	60.4	147	3	US-09-539-443-4
93	55	60.4	147	4	US-10-627-829-4
94	54	59.3	16	3	US-09-539-443-40
95	54	59.3	16	3	US-09-539-443-64
96	54	59.3	16	4	US-10-627-829-40
97	54	59.3	16	4	US-10-627-829-64
98	54	59.3	17	3	US-09-865-943-97
99	54	59.3	18	3	US-09-030-619-223
100	54	59.3	18	3	US-09-912-609-111

Sequence 59, Appl  
Sequence 221, App  
Sequence 109, App  
Sequence 11, Appl  
Sequence 16, Appl  
Sequence 33, Appl  
Sequence 48, Appl  
Sequence 15, Appl  
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Sequence 32, Appl  
Sequence 33, Appl  
Sequence 15, Appl  
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Sequence 15, Appl  
Sequence 11, Appl  
Sequence 16, Appl  
Sequence 33, Appl  
Sequence 48, Appl  
Sequence 15, App  
Sequence 1019, App  
Sequence 102, App  
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Sequence 17, Appl  
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Sequence 32, Appl  
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Sequence 2, Appl  
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Sequence 46, Appl  
Sequence 37, Appl  
Sequence 45, Appl  
Sequence 60, Appl  
Sequence 185, App  
Sequence 8, Appl  
Sequence 46, Appl  
Sequence 55, Appl  
Sequence 57, Appl  
Sequence 60, Appl  
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Sequence 9, Appl  
Sequence 34, Appl  
Sequence 35, Appl  
Sequence 36, Appl  
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Sequence 55, Appl  
Sequence 57, Appl  
Sequence 60, Appl  
Sequence 62, Appl  
Sequence 19, Appl  
Sequence 68, Appl  
Sequence 88, Appl  
Sequence 191, App  
Sequence 39, Appl  
Sequence 49, Appl  
Sequence 39, Appl  
Sequence 49, Appl  
Sequence 4, Appl  
Sequence 40, Appl  
Sequence 64, Appl  
Sequence 40, Appl  
Sequence 64, Appl  
Sequence 97, Appl  
Sequence 223, App  
Sequence 111, App

## ALIGNMENTS

RESULT 1  
US-10-336-312-1  
; Sequence 1, Application US/10336312  
; Publication No. US20030186890A1  
; GENERAL INFORMATION:  
; APPLICANT: DRIN, GUILLAUME  
; APPLICANT: GOMAR, JEROME  
; APPLICANT: TEMSAMANI, JAMAL  
; APPLICANT: REES, ANTHONY B.  
; TITLE OF INVENTION: AMPHIPHATIC LINEAR PEPTIDES AND FORMULATIONS CONTAINING  
; FILE REFERENCE: 1534-02  
; CURRENT APPLICATION NUMBER: US/10/336,312  
; PRIOR FILING DATE: 2003-02-27  
; PRIOR APPLICATION NUMBER: PCT/FR01/02129  
; PRIOR FILING DATE: 2001-07-03  
; PRIOR APPLICATION NUMBER: FR 00/08633  
; NUMBER OF SEQ ID NOS: 52  
; SOFTWARE: PatentIn Ver. 2.1  
; SEQ ID NO 1  
; LENGTH: 18  
; TYPE: PRT  
; ORGANISM: Unknown Organism  
; FEATURE:  
; OTHER INFORMATION: Description of Unknown Organism: Peptide SynB1  
US-10-336-312-1  
Query Match 100.0%; Score 91; DB 4; Length 18;  
Best Local Similarity 100.0%; Pred. No. 2.1e-07;  
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
QY 1 RGGRLSYRRRFFSTSTGR 18  
DB 1 RGGRLSYRRRFFSTSTGR 18  
RESULT 2  
US-10-136-187-24  
; Sequence 24, Application US/10136187  
; Publication No. US20030203865A1  
; GENERAL INFORMATION:  
; APPLICANT: Harvie, Pierrot  
; APPLICANT: Paul, Ralph  
; APPLICANT: Cudmore, Sally  
; APPLICANT: O'Mahony, Daniel J.  
; TITLE OF INVENTION: LIPID-COMPRISING DRUG DELIVERY COMPLEXES  
; FILE REFERENCE: 226272005300  
; CURRENT APPLICATION NUMBER: US/10/136,187  
; CURRENT FILING DATE: 2002-09-13  
; PRIOR APPLICATION NUMBER: US 60/287,786  
; PRIOR FILING DATE: 2001-04-30  
; NUMBER OF SEQ ID NOS: 45  
; SOFTWARE: FastSeq for Windows Version 4.0  
; SEQ ID NO 24  
; LENGTH: 18  
; TYPE: PRT  
; ORGANISM: Artificial Sequence  
; FEATURE:  
; OTHER INFORMATION: Synthetic Construct  
US-10-136-187-24  
Query Match 100.0%; Score 91; DB 4; Length 18;  
Best Local Similarity 100.0%; Pred. No. 2.1e-07;  
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
QY 1 RGGRLSYRRRFFSTSTGR 18

DB 1 RGGRLSYRRRFFSTSTGR 18  
RESULT 3  
US-10-144-549-17  
; Sequence 17, Application US/10144549  
; Publication No. US20030211590A1  
; GENERAL INFORMATION:  
; APPLICANT: Geneshuttle Biopharm, Inc.  
; APPLICANT: Hwu, Paul L.  
; TITLE OF INVENTION: A NEW FUSION PROTEIN FOR USE AS VECTOR  
; FILE REFERENCE: MHB 02-340  
; CURRENT APPLICATION NUMBER: US/10/144,549  
; CURRENT FILING DATE: 2002-05-13  
; NUMBER OF SEQ ID NOS: 31  
; SOFTWARE: PatentIn version 3.1  
; SEQ ID NO 17  
; LENGTH: 18  
; TYPE: PRT  
; ORGANISM: Artificial Sequence  
; FEATURE:  
; OTHER INFORMATION: Membrane fusion sequence.  
; NAME/KEY: MISC FEATURE  
; OTHER INFORMATION: Synthetic sequence from protegrins/procine leukocyte.  
US-10-144-549-17  
Query Match 100.0%; Score 91; DB 4; Length 18;  
Best Local Similarity 100.0%; Pred. No. 2.1e-07;  
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
QY 1 RGGRLSYRRRFFSTSTGR 18  
DB 1 RGGRLSYRRRFFSTSTGR 18  
RESULT 4  
US-10-185-593-3  
; Sequence 3, Application US/10185593  
; Publication No. US20030220474A1  
; GENERAL INFORMATION:  
; APPLICANT: PACIFIC CORPORATION  
; TITLE OF INVENTION: Conjugate of biodegradable aliphatic polyester with Tat49-57  
; FILE REFERENCE: 2002dp109  
; CURRENT APPLICATION NUMBER: US/10/185,593  
; CURRENT FILING DATE: 2002-06-28  
; NUMBER OF SEQ ID NOS: 6  
; SOFTWARE: KopatentIn 1.71  
; SEQ ID NO 3  
; LENGTH: 18  
; TYPE: PRT  
; ORGANISM: Artificial Sequence  
; FEATURE:  
; OTHER INFORMATION: peptide derived from SynB1 of protegrins  
US-10-185-593-3  
Query Match 100.0%; Score 91; DB 4; Length 18;  
Best Local Similarity 100.0%; Pred. No. 2.1e-07;  
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
QY 1 RGGRLSYRRRFFSTSTGR 18  
DB 1 RGGRLSYRRRFFSTSTGR 18  
RESULT 5  
US-10-270-010-10  
; Sequence 10, Application US/10270010  
; Publication No. US20040072340A1  
; GENERAL INFORMATION:

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; APPLICANT: Johnson, Mark Elliott
; APPLICANT: Hamilton Day, Fiona
; APPLICANT: Kaczorek, Michel
; APPLICANT: Tensamani, Jamal
; TITLE OF INVENTION: Use of peptide vectors to improve the immune response
; TITLE OF INVENTION: to antigens
; FILE REFERENCE:
; CURRENT APPLICATION NUMBER: US/10/270,010
; CURRENT FILING DATE: 2002-10-15
; PRIOR APPLICATION NUMBER: EP 01402671.0
; PRIOR FILING DATE: 2001-10-16
; NUMBER OF SEQ ID NOS: 22
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 10
; LENGTH: 18
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Linear
; OTHER INFORMATION: derivative of a beta-stranded antibiotic peptide
US-10-270-010-10

Query Match          100.0%; Score 91; DB 4; Length 18;
Best Local Similarity 100.0%; Pred. No. 2.1e-07;
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 RGGRLSYRRRFFSTGCR 18
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Db 1 RGGRLSYRRRFFSTGCR 18

RESULT 6
US-10-850-873-24
; Sequence 24, Application US/10850873
; Publication No. US20050025821A1
; GENERAL INFORMATION:
; APPLICANT: Harvie, Pierrot
; APPLICANT: Paul, Ralph
; APPLICANT: Cudmore, Sally
; APPLICANT: O'Mahony, Daniel J.
; TITLE OF INVENTION: LIPID-COMPISING DRUG DELIVERY COMPLEXES
; TITLE OF INVENTION: AND METHODS FOR THEIR PRODUCTION
; FILE REFERENCE: 226272005300
; CURRENT APPLICATION NUMBER: US/10/850,873
; CURRENT FILING DATE: 2004-05-20
; PRIOR APPLICATION NUMBER: US/10/136,187
; PRIOR FILING DATE: 2002-04-30
; PRIOR APPLICATION NUMBER: US 60/287,786
; PRIOR FILING DATE: 2001-04-30
; NUMBER OF SEQ ID NOS: 45
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 24
; LENGTH: 18
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Synthetic Construct
US-10-850-873-24

Query Match          100.0%; Score 91; DB 5; Length 18;
Best Local Similarity 100.0%; Pred. No. 2.1e-07;
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 RGGRLSYRRRFFSTGCR 18
   |||||
Db 1 RGGRLSYRRRFFSTGCR 18

RESULT 7
US-10-878-175B-36
; Sequence 36, Application US/10878175B
; Publication No. US20050153913A1
; GENERAL INFORMATION:
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; APPLICANT: Kosak, Kenneth M.
; TITLE OF INVENTION: Nucleic Acid Carrier Compositions and Methods for Their Synthesis
; FILE REFERENCE: Confirmation No. 5281
; CURRENT APPLICATION NUMBER: US/10/878,175B
; CURRENT FILING DATE: 2004-06-28
; NUMBER OF SEQ ID NOS: 51
; SOFTWARE: PatentIn version 3.3
; SEQ ID NO 36
; LENGTH: 18
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Table I Transduction Peptide
US-10-878-175B-36

Query Match          100.0%; Score 91; DB 5; Length 18;
Best Local Similarity 100.0%; Pred. No. 2.1e-07;
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 RGGRLSYRRRFFSTGCR 18
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Db 1 RGGRLSYRRRFFSTGCR 18

RESULT 8
US-10-923-112A-36
; Sequence 36, Application US/10923112A
; Publication No. US20060040879A1
; GENERAL INFORMATION:
; APPLICANT: Kosak, Kenneth M.
; TITLE OF INVENTION: Chloroquine Coupled Nucleic Acids and Methods for Their Synthesis
; FILE REFERENCE: Confirmation No. 3293
; CURRENT APPLICATION NUMBER: US/10/923,112A
; CURRENT FILING DATE: 2004-08-21
; NUMBER OF SEQ ID NOS: 54
; SOFTWARE: PatentIn version 3.3
; SEQ ID NO 36
; LENGTH: 18
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Table I Transduction Peptide
US-10-923-112A-36

Query Match          100.0%; Score 91; DB 5; Length 18;
Best Local Similarity 100.0%; Pred. No. 2.1e-07;
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 RGGRLSYRRRFFSTGCR 18
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Db 1 RGGRLSYRRRFFSTGCR 18

RESULT 9
US-11-027-967-3
; Sequence 3, Application US/11027967
; Publication No. US20050112089A1
; GENERAL INFORMATION:
; APPLICANT: PACIFIC CORPORATION
; TITLE OF INVENTION: Conjugate of biodegradable aliphatic polyester with Tat49-57
; TITLE OF INVENTION: peptide or peptide chain containing Tat49-57 peptide, and
; TITLE OF INVENTION: nanoparticle manufactured using the same
; FILE REFERENCE: 2002dp109
; CURRENT APPLICATION NUMBER: US/11/027,967
; CURRENT FILING DATE: 2005-01-03
; PRIOR APPLICATION NUMBER: US/10/185,593
; PRIOR FILING DATE: 2002-06-28
; NUMBER OF SEQ ID NOS: 6
; SOFTWARE: Kopatentin 1.71
; SEQ ID NO 3
; LENGTH: 18
; TYPE: PRT
; ORGANISM: Artificial Sequence
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; FEATURE:  
; OTHER INFORMATION: peptide derived from SynB1 of protegrins  
US-11-027-967-3

Query Match 100.0%; Score 91; DB 6; Length 18;  
Best Local Similarity 100.0%; Pred. No. 2.1e-07;  
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 RGRLSYSRRRSTSTGR 18  
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DB 1 RGRLSYSRRRSTSTGR 18

RESULT 10  
US-10-270-010-7  
; Sequence 7, Application US/10270010  
; Publication No. US20040072340A1  
; GENERAL INFORMATION:  
; APPLICANT: Johnson, Mark Elliott  
; APPLICANT: Hamilton Day, Piona  
; APPLICANT: Kaczorek, Michel  
; APPLICANT: Temsamani, Jamal  
; TITLE OF INVENTION: Use of peptide vectors to improve the immune response  
; FILE REFERENCE:  
; CURRENT APPLICATION NUMBER: US/10/270,010  
; CURRENT FILING DATE: 2002-10-15  
; PRIOR APPLICATION NUMBER: EP 01402671.0  
; PRIOR FILING DATE: 2001-10-16  
; NUMBER OF SEQ ID NOS: 22  
; SOFTWARE: PatentIn Ver. 2.1  
; SEQ ID NO 7  
; LENGTH: 18  
; TYPE: PRT  
; ORGANISM: Artificial Sequence  
; FEATURE:  
; OTHER INFORMATION: Description of Artificial Sequence: Linear  
; OTHER INFORMATION: derivative of a beta-stranded antibiotic peptide  
US-10-270-010-7

Query Match 89.0%; Score 81; DB 4; Length 18;  
Best Local Similarity 88.9%; Pred. No. 8.3e-06;  
Matches 16; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1 RGRLSYSRRRSTSTGR 18  
| | | | | | | | | | | | | | | | | |  
DB 1 RGRLSYSRRRSTSVGR 18

RESULT 11  
US-10-500-671A-15  
; Sequence 15, Application US/10500671A  
; Publication No. US20050170348A1  
; GENERAL INFORMATION:  
; APPLICANT: Sera, Takashi  
; TITLE OF INVENTION: Nuclear-Envelope and Nuclear-Lamina Binding Chimeras for  
; FILE REFERENCE: 109845-163  
; CURRENT APPLICATION NUMBER: US/10/500,671A  
; CURRENT FILING DATE: 2004-07-02  
; NUMBER OF SEQ ID NOS: 21  
; SOFTWARE: PatentIn version 3.3  
; SEQ ID NO 15  
; LENGTH: 16  
; TYPE: PRT  
; ORGANISM: Artificial  
; FEATURE:  
; OTHER INFORMATION: Peptide Syn B1 from Antennapedia homeodomain protein  
US-10-500-671A-15

Query Match 87.9%; Score 80; DB 5; Length 16;  
Best Local Similarity 100.0%; Pred. No. 1.1e-05;  
Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 RGRLSYSRRRSTST 16  
| | | | | | | | | | | | | | | | | |  
DB 1 RGRLSYSRRRSTST 16

RESULT 12  
US-09-810-601-42  
; Sequence 42, Application US/09810601  
; Patent No. US20020177545A1  
; GENERAL INFORMATION:  
; APPLICANT: Donovan, Stephen  
; TITLE OF INVENTION: Compositions and Methods for Treating Gonadotrophin  
; FILE REFERENCE: 2947  
; CURRENT APPLICATION NUMBER: US/09/810,601  
; CURRENT FILING DATE: 2001-03-15  
; NUMBER OF SEQ ID NOS: 44  
; SOFTWARE: PatentIn Ver. 2.1  
; SEQ ID NO 42  
; LENGTH: 18  
; TYPE: PRT  
; ORGANISM: Artificial Sequence  
; FEATURE:  
; OTHER INFORMATION: Description of Artificial Sequence: Membrane  
; OTHER INFORMATION: Translocation Peptide  
; PUBLICATION INFORMATION:  
; AUTHORS: Rousselle, Christophe  
; JOURNAL: Mol. Pharmacol.  
; VOLUME: 57  
; PAGES: 679-686  
; DATE: 2000  
US-09-810-601-42

Query Match 87.9%; Score 80; DB 3; Length 18;  
Best Local Similarity 88.9%; Pred. No. 1.2e-05;  
Matches 16; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 1 RGRLSYSRRRSTSTGR 18  
| | | | | | | | | | | | | | | | | |  
DB 1 RGRKSWRRRSTSTGR 18

RESULT 13  
US-10-336-312-26  
; Sequence 26, Application US/10336312  
; Publication No. US20030186890A1  
; GENERAL INFORMATION:  
; APPLICANT: DRIN, GUILLAUME  
; APPLICANT: GOMAR, JEROME  
; APPLICANT: TEMSAMANI, JAMAL  
; APPLICANT: REES, ANTHONY B.  
; TITLE OF INVENTION: AMPHIPATHIC LINEAR PEPTIDES AND FORMULATIONS CONTAINING  
; FILE REFERENCE: 1534-02  
; CURRENT APPLICATION NUMBER: US/10/336,312  
; CURRENT FILING DATE: 2003-02-27  
; PRIOR APPLICATION NUMBER: PCT/FR01/02129  
; PRIOR FILING DATE: 2001-07-03  
; PRIOR APPLICATION NUMBER: FR 00/08633  
; PRIOR FILING DATE: 2000-07-03  
; NUMBER OF SEQ ID NOS: 52  
; SOFTWARE: PatentIn Ver. 2.1  
; SEQ ID NO 26  
; LENGTH: 18  
; TYPE: PRT  
; ORGANISM: Artificial Sequence  
; FEATURE:  
; OTHER INFORMATION: Description of Artificial Sequence: Synthetic  
; OTHER INFORMATION: peptide SynB/2cit  
; FEATURE:  
; NAME/KEY: MOD\_RES  
; LOCATION: (9)..(10)

QY 1 RGRLSYSRRRSTSTGR 18  
| | | | | | | | | | | | | | | | | |  
DB 1 RGRKSWRRRSTSTGR 18

RESULT 13  
US-10-336-312-26  
; Sequence 26, Application US/10336312  
; Publication No. US20030186890A1  
; GENERAL INFORMATION:  
; APPLICANT: DRIN, GUILLAUME  
; APPLICANT: GOMAR, JEROME  
; APPLICANT: TEMSAMANI, JAMAL  
; APPLICANT: REES, ANTHONY B.  
; TITLE OF INVENTION: AMPHIPATHIC LINEAR PEPTIDES AND FORMULATIONS CONTAINING  
; FILE REFERENCE: 1534-02  
; CURRENT APPLICATION NUMBER: US/10/336,312  
; CURRENT FILING DATE: 2003-02-27  
; PRIOR APPLICATION NUMBER: PCT/FR01/02129  
; PRIOR FILING DATE: 2001-07-03  
; PRIOR APPLICATION NUMBER: FR 00/08633  
; PRIOR FILING DATE: 2000-07-03  
; NUMBER OF SEQ ID NOS: 52  
; SOFTWARE: PatentIn Ver. 2.1  
; SEQ ID NO 26  
; LENGTH: 18  
; TYPE: PRT  
; ORGANISM: Artificial Sequence  
; FEATURE:  
; OTHER INFORMATION: Description of Artificial Sequence: Synthetic  
; OTHER INFORMATION: peptide SynB/2cit  
; FEATURE:  
; NAME/KEY: MOD\_RES  
; LOCATION: (9)..(10)

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; OTHER INFORMATION: Citrulline
US-10-336-312-26
Query Match      86.8%; Score 79; DB 4; Length 18;
Best Local Similarity 88.9%; Pred. No. 1.7e-05;
Matches 16; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 1 RGGRLSYRRRRFSTSTGR 18
    |||||  |||||
Db 1 RGGRLSYRRRRFSTSTGR 18

RESULT 14
US-10-336-312-27
; Sequence 27, Application US/10336312
; Publication No. US20030186890A1
; GENERAL INFORMATION:
; APPLICANT: DRIN, GUILLAUME
; APPLICANT: GOMAR, JEROME
; APPLICANT: TEMSAMANI, JAMAL
; TITLE OF INVENTION: AMPHIPATHIC LINEAR PEPTIDES AND FORMULATIONS CONTAINING
; TITLE OF INVENTION: SAID PEPTIDES
; FILE REFERENCE: 1534-02
; CURRENT APPLICATION NUMBER: US/10/336,312
; PRIOR FILING DATE: 2003-02-27
; PRIOR APPLICATION NUMBER: PCT/FR01/02129
; PRIOR FILING DATE: 2001-07-03
; PRIOR APPLICATION NUMBER: FR 00/08633
; PRIOR FILING DATE: 2000-07-03
; NUMBER OF SEQ ID NOS: 52
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 27
; LENGTH: 18
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Synthetic
; OTHER INFORMATION: peptide SynBl/3cit
; NAME/KEY: MOD RES
; LOCATION: (9)..(11)
; OTHER INFORMATION: Citrulline
US-10-336-312-27

Query Match      80.2%; Score 73; DB 4; Length 18;
Best Local Similarity 83.3%; Pred. No. 0.00016;
Matches 15; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Qy 1 RGGRLSYRRRRFSTSTGR 18
    |||||  |||||
Db 1 RGGRLSYRRRRFSTSTGR 18

RESULT 16
US-10-336-312-7
; Sequence 7, Application US/10336312
; Publication No. US20030186890A1
; GENERAL INFORMATION:
; APPLICANT: DRIN, GUILLAUME
; APPLICANT: GOMAR, JEROME
; APPLICANT: TEMSAMANI, JAMAL
; TITLE OF INVENTION: AMPHIPATHIC LINEAR PEPTIDES AND FORMULATIONS CONTAINING
; TITLE OF INVENTION: SAID PEPTIDES
; FILE REFERENCE: 1534-02
; CURRENT APPLICATION NUMBER: US/10/336,312
; PRIOR FILING DATE: 2003-02-27
; PRIOR APPLICATION NUMBER: PCT/FR01/02129
; PRIOR FILING DATE: 2001-07-03
; PRIOR APPLICATION NUMBER: FR 00/08633
; PRIOR FILING DATE: 2000-07-03
; NUMBER OF SEQ ID NOS: 52
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 7
; LENGTH: 18
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Synthetic
; OTHER INFORMATION: peptide PG-4A
US-10-336-312-7

Query Match      75.8%; Score 69; DB 4; Length 18;
Best Local Similarity 66.7%; Pred. No. 0.00067;
Matches 12; Conservative 4; Mismatches 2; Indels 0; Gaps 0;

Qy 1 RGGRLSYRRRRFSTSTGR 18
    |||||  |||||
Db 1 RGGRLSYRRRRFSTSTGR 18

RESULT 17
US-09-539-443-63
; Sequence 63, Application US/09539443
; Publication No. US20030100483A1
; GENERAL INFORMATION:
; APPLICANT: LEHRER, ROBERT I.
; APPLICANT: HARWIG, SYLVIA S.L.
; APPLICANT: KOKRYAKOV, VLADIMIR N.
; TITLE OF INVENTION: PROTEGRINS
; NUMBER OF SEQUENCES: 76
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: PENNIE & EDMONDS LLP
```

STREET: 1155 Avenue of the Americas  
CITY: New York  
STATE: New York  
COUNTRY: USA  
ZIP: 10036-2711  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: PatentIn Release #1.0, Version #1.30  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/09/539,443  
FILING DATE: 30-MARCH-2000  
CLASSIFICATION:  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US/09/128,345  
FILING DATE: 03-AUG-1998  
ATTORNEY/AGENT INFORMATION:  
NAME: Coruzzi, Laura, A.  
REGISTRATION NUMBER: 30,742  
REFERENCE/DOCKET NUMBER: 8067-0054-999  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (212) 790-9090  
TELEFAX: (212) 869-9741  
INFORMATION FOR SEQ ID NO: 63:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 18 amino acids  
TYPE: amino acid  
STRANDEDNESS: single  
TOPOLOGY: linear  
NAME/KEY: Modified-site  
LOCATION: group(6, 8, 13, 15)  
OTHER INFORMATION: /note= "X is a hydrophobic, a  
OTHER INFORMATION: small, or a large polar amino acid"  
US-09-539-443-63

Query Match 71.4%; Score 65; DB 3; Length 18;  
Best Local Similarity 66.7%; Pred. No. 0.0029;  
Matches 12; Conservative 0; Mismatches 6; Indels 0;

QY 1 RGGRLSYRRRFRSTGTGR 18  
Db 1 RGGRLXXRRRFXVXVGR 18

RESULT 18  
US-09-539-443-67  
Sequence 67, Application US/09539443  
Publication No. US20030100483A1  
GENERAL INFORMATION:  
APPLICANT: LEHRER, ROBERT I.  
APPLICANT: HARWIG, SYLVIA S.L.  
APPLICANT: KOKRYAKOV, VLADIMIR N.  
TITLE OF INVENTION: PROTEGRINS  
NUMBER OF SEQUENCES: 76  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: PENNIE & EDMONDS LLP  
STREET: 1155 Avenue of the Americas  
CITY: New York  
STATE: New York  
COUNTRY: USA  
ZIP: 10036-2711  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: PatentIn Release #1.0, Version #1.30  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/09/539,443  
FILING DATE: 30-MARCH-2000  
CLASSIFICATION:

PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US/09/128,345  
FILING DATE: 03-AUG-1998  
ATTORNEY/AGENT INFORMATION:  
NAME: Coruzzi, Laura, A.  
REGISTRATION NUMBER: 30,742  
REFERENCE/DOCKET NUMBER: 8067-0054-999  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (212) 790-9090  
TELEFAX: (212) 869-9741  
INFORMATION FOR SEQ ID NO: 67:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 18 amino acids  
TYPE: amino acid  
STRANDEDNESS: single  
TOPOLOGY: linear  
NAME/KEY: Modified-site  
LOCATION: group(6, 8, 13, 15)  
OTHER INFORMATION: /note= "X is a hydrophobic, a  
OTHER INFORMATION: small, or a large polar amino acid"  
US-09-539-443-67

Query Match 71.4%; Score 65; DB 3; Length 18;  
Best Local Similarity 66.7%; Pred. No. 0.0029;  
Matches 12; Conservative 0; Mismatches 6; Indels 0;

QY 1 RGGRLSYRRRFRSTGTGR 18  
Db 1 RGGRLXXRRRFXVXVGR 18

RESULT 19  
US-10-627-829-63  
Sequence 63, Application US/10627829  
Publication No. US20040152638A1  
GENERAL INFORMATION:  
APPLICANT: LEHRER, ROBERT I.  
APPLICANT: HARWIG, SYLVIA S.L.  
APPLICANT: KOKRYAKOV, VLADIMIR N.  
TITLE OF INVENTION: PROTEGRINS  
NUMBER OF SEQUENCES: 76  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: PENNIE & EDMONDS LLP  
STREET: 1155 Avenue of the Americas  
CITY: New York  
STATE: New York  
COUNTRY: USA  
ZIP: 10036-2711  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: PatentIn Release #1.0, Version #1.30  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/10/627,829  
FILING DATE: 24-JULY-2003  
CLASSIFICATION:  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US/09/539,443  
FILING DATE: 30-MARCH-2000  
APPLICATION NUMBER: US/09/128,345  
FILING DATE: 03-AUG-1998  
ATTORNEY/AGENT INFORMATION:  
NAME: Coruzzi, Laura, A.  
REGISTRATION NUMBER: 30,742  
REFERENCE/DOCKET NUMBER: 8067-0054-999  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (212) 790-9090  
TELEFAX: (212) 869-9741  
INFORMATION FOR SEQ ID NO: 63:

SEQUENCE CHARACTERISTICS:  
LENGTH: 18 amino acids  
TYPE: amino acid  
STRANDEDNESS: single  
TOPOLOGY: linear  
FEATURE:  
NAME/KEY: Modified-site  
LOCATION: group(6, 8, 13, 15)  
OTHER INFORMATION: /note= "X is a hydrophobic, a  
OTHER INFORMATION: small, or a large polar amino acid"  
US-10-627-829-63

Query Match 71.4%; Score 65; DB 4; Length 18;  
Best Local Similarity 66.7%; Pred. No. 0.0029;  
Matches 12; Conservative 0; Mismatches 6; Indels 0; Gaps 0;

QY 1 RGGRLSYRRRFFSTGTGR 18  
|||||  
Db 1 RGGRLXYRRRFFXVXVGR 18

## RESULT 20

US-10-627-829-67  
Sequence 67, Application US/10627829  
Publication No. US20040152638A1  
GENERAL INFORMATION:  
APPLICANT: LEHRER, ROBERT I.  
APPLICANT: HARWIG, SYLVIA S.L.  
APPLICANT: KOKRYAKOV, VLADIMIR N.  
TITLE OF INVENTION: PROTEGRINS  
NUMBER OF SEQUENCES: 76  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: PENNIE & EDMONDS LLP  
STREET: 1155 Avenue of the Americas  
CITY: New York  
STATE: New York  
COUNTRY: USA  
ZIP: 10036-2711  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: PatentIn Release #1.0, Version #1.30  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/10/627,829  
FILING DATE: 24-JULY-2003  
CLASSIFICATION:  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US/09/539,443  
FILING DATE: 30-MARCH-2000  
APPLICATION NUMBER: US/09/128,345  
FILING DATE: 03-AUG-1998  
ATTORNEY/AGENT INFORMATION:  
NAME: Coruzzi, Laura, A.  
REGISTRATION NUMBER: 30,742  
REFERENCE/DOCKET NUMBER: 8067-0054-999  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (212) 790-9090  
TELEFAX: (212) 869-9741  
TELEX: 66141 PENNIE  
INFORMATION FOR SEQ ID NO: 67:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 18 amino acids  
TYPE: amino acid  
STRANDEDNESS: single  
TOPOLOGY: linear  
FEATURE:  
NAME/KEY: Modified-site  
LOCATION: group(6, 8, 13, 15)  
OTHER INFORMATION: /note= "X is a hydrophobic, a  
OTHER INFORMATION: small, or a large polar amino acid"  
US-10-627-829-67

Query Match 71.4%; Score 65; DB 4; Length 18;  
Best Local Similarity 66.7%; Pred. No. 0.0029;  
Matches 12; Conservative 0; Mismatches 6; Indels 0; Gaps 0;

QY 1 RGGRLSYRRRFFSTGTGR 18  
|||||  
Db 1 RGGRLXYRRRFFXVXVGR 18

## RESULT 21

US-09-539-443-53  
Sequence 53, Application US/09539443  
Publication No. US20030100483A1  
GENERAL INFORMATION:  
APPLICANT: LEHRER, ROBERT I.  
APPLICANT: HARWIG, SYLVIA S.L.  
APPLICANT: KOKRYAKOV, VLADIMIR N.  
TITLE OF INVENTION: PROTEGRINS  
NUMBER OF SEQUENCES: 76  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: PENNIE & EDMONDS LLP  
STREET: 1155 Avenue of the Americas  
CITY: New York  
STATE: New York  
COUNTRY: USA  
ZIP: 10036-2711  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: PatentIn Release #1.0, Version #1.30  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/09/539,443  
FILING DATE: 30-MARCH-2000  
CLASSIFICATION:  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US/09/128,345  
FILING DATE: 03-AUG-1998  
ATTORNEY/AGENT INFORMATION:  
NAME: Coruzzi, Laura, A.  
REGISTRATION NUMBER: 30,742  
REFERENCE/DOCKET NUMBER: 8067-0054-999  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (212) 790-9090  
TELEFAX: (212) 869-9741  
TELEX: 66141 PENNIE  
INFORMATION FOR SEQ ID NO: 53:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 18 amino acids  
TYPE: amino acid  
STRANDEDNESS: single  
TOPOLOGY: linear  
FEATURE:  
NAME/KEY: Disulfide-bond  
LOCATION: 8..13  
FEATURE:  
NAME/KEY: Modified-site  
LOCATION: group(6, 15)  
OTHER INFORMATION: /note= "X is a hydrophobic, a  
OTHER INFORMATION: small, or a large polar amino acid"  
US-09-539-443-53

Query Match 69.2%; Score 63; DB 3; Length 18;  
Best Local Similarity 66.7%; Pred. No. 0.0061;  
Matches 12; Conservative 0; Mismatches 6; Indels 0; Gaps 0;

QY 1 RGGRLSYRRRFFSTGTGR 18  
|||||  
Db 1 RGGRLXYRRRFFXVXVGR 18

## RESULT 22

US-09-539-443-58

; Sequence 58, Application US/09539443  
; Publication No. US20030100483A1  
; GENERAL INFORMATION:  
; APPLICANT: LEHRER, ROBERT I.  
; APPLICANT: HARWIG, SYLVIA S.L.  
; APPLICANT: KOKRYAKOV, VLADIMIR N.  
; TITLE OF INVENTION: PROTEGRINS  
; NUMBER OF SEQUENCES: 76  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: PENNIE & EDMONDS LLP  
; STREET: 1155 Avenue of the Americas  
; CITY: New York  
; STATE: New York  
; COUNTRY: USA  
; ZIP: 10036-2711  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Floppy disk  
; COMPUTER: IBM PC compatible  
; OPERATING SYSTEM: PC-DOS/MS-DOS  
; SOFTWARE: PatentIn Release #1.0, Version #1.30  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/09/539,443  
; FILING DATE: 30-MARCH-2000  
; CLASSIFICATION:  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: US/09/128,345  
; FILING DATE: 03-AUG-1998  
; ATTORNEY/AGENT INFORMATION:  
; NAME: Coruzzi, Laura, A.  
; REGISTRATION NUMBER: 30,742  
; REFERENCE/DOCKET NUMBER: 8067-0054-999  
; TELEPHONE: (212) 790-9090  
; TELEFAX: (212) 869-9741  
; INFORMATION FOR SEQ ID NO: 58:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 18 amino acids  
; TYPE: amino acid  
; STRANDEDNESS: single  
; TOPOLOGY: linear  
; FEATURE:  
; NAME/KEY: Disulfide-bond  
; LOCATION: 6..15  
; FEATURE:  
; NAME/KEY: Modified-site  
; LOCATION: group(8, 13)  
; OTHER INFORMATION: /note= "X is a hydrophobic, a  
; OTHER INFORMATION: small, or a large polar amino acid"  
; US-09-539-443-58

Query Match 69.2%; Score 63; DB 3; Length 18;  
Best Local Similarity 66.7%; Pred. No. 0.0061;  
Matches 12; Conservative 0; Mismatches 6; Indels 0; Gaps 0;

QY 1 RGGRLSYRRRSTSTGR 18  
|||||  
DB 1 RGGRLCYRRRFXCVGR 18

RESULT 23  
US-10-627-829-53  
; Sequence 53, Application US/10627829  
; Publication No. US20040152638A1  
; GENERAL INFORMATION:  
; APPLICANT: LEHRER, ROBERT I.  
; APPLICANT: HARWIG, SYLVIA S.L.  
; APPLICANT: KOKRYAKOV, VLADIMIR N.  
; TITLE OF INVENTION: PROTEGRINS  
; NUMBER OF SEQUENCES: 76  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: PENNIE & EDMONDS LLP  
; STREET: 1155 Avenue of the Americas

; CITY: New York  
; STATE: New York  
; COUNTRY: USA  
; ZIP: 10036-2711  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Floppy disk  
; COMPUTER: IBM PC compatible  
; OPERATING SYSTEM: PC-DOS/MS-DOS  
; SOFTWARE: PatentIn Release #1.0, Version #1.30  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/10/627,829  
; FILING DATE: 24-JULY-2003  
; CLASSIFICATION:  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: US/09/539,443  
; FILING DATE: 30-MARCH-2000  
; APPLICATION NUMBER: US/09/128,345  
; FILING DATE: 03-AUG-1998  
; ATTORNEY/AGENT INFORMATION:  
; NAME: Coruzzi, Laura, A.  
; REGISTRATION NUMBER: 30,742  
; REFERENCE/DOCKET NUMBER: 8067-0054-999  
; TELEPHONE: (212) 790-9090  
; TELEFAX: (212) 869-9741  
; INFORMATION FOR SEQ ID NO: 53:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 18 amino acids  
; TYPE: amino acid  
; STRANDEDNESS: single  
; TOPOLOGY: linear  
; FEATURE:  
; NAME/KEY: Disulfide-bond  
; LOCATION: 8..13  
; FEATURE:  
; NAME/KEY: Modified-site  
; LOCATION: group(6, 15)  
; OTHER INFORMATION: /note= "X is a hydrophobic, a  
; OTHER INFORMATION: small, or a large polar amino acid"  
; US-10-627-829-53

Query Match 69.2%; Score 63; DB 4; Length 18;  
Best Local Similarity 66.7%; Pred. No. 0.0061;  
Matches 12; Conservative 0; Mismatches 6; Indels 0; Gaps 0;

QY 1 RGGRLSYRRRSTSTGR 18  
|||||  
DB 1 RGGRLCYRRRFXCVGR 18

RESULT 24  
US-10-627-829-58  
; Sequence 58, Application US/10627829  
; Publication No. US20040152638A1  
; GENERAL INFORMATION:  
; APPLICANT: LEHRER, ROBERT I.  
; APPLICANT: HARWIG, SYLVIA S.L.  
; APPLICANT: KOKRYAKOV, VLADIMIR N.  
; TITLE OF INVENTION: PROTEGRINS  
; NUMBER OF SEQUENCES: 76  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: PENNIE & EDMONDS LLP  
; STREET: 1155 Avenue of the Americas  
; CITY: New York  
; STATE: New York  
; COUNTRY: USA  
; ZIP: 10036-2711  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Floppy disk  
; COMPUTER: IBM PC compatible  
; OPERATING SYSTEM: PC-DOS/MS-DOS  
; SOFTWARE: PatentIn Release #1.0, Version #1.30



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; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/10/627,829
; FILING DATE: 24-JULY-2003
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US/09/539,443
; FILING DATE: 30-MARCH-2000
; APPLICATION NUMBER: US/09/128,345
; FILING DATE: 03-AUG-1998
; ATTORNEY/AGENT INFORMATION:
; NAME: Coruzzi, Laura, A.
; REGISTRATION NUMBER: 30,742
; REFERENCE/DOCKET NUMBER: 8067-0054-999
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (212) 790-9090
; TELEFAX: (212) 869-9741
; TELEX: 66141 PENNIE
; INFORMATION FOR SEQ ID NO: 58:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 18 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; NAME/KEY: Disulfide-bond
; LOCATION: 6..15
; FEATURES:
; NAME/KEY: Modified-eite
; LOCATION: group(8, 13)
; OTHER INFORMATION: /note= "X is a hydrophobic, a
; OTHER INFORMATION: small, or a large polar amino acid"
;
US-10-627-829-58

```

```

Query Match 69.2%; Score 63; DB 4; Length 18;
Best Local Similarity 66.7%; Pred. No. 0.0061;
Matches 12; Conservative 0; Mismatches 6; Indels 0; Gaps 0;

```

```

Qy 1 RGGRLSYRRRPFSTGCR 18
    ||||| ||||| ||
Db 1 RGGRLCYRRRFXVCVGR 18

```

```

RESULT 25
US-09-539-443-54
; Sequence 54, Application US/09539443
; Publication No. US20030100483A1
; GENERAL INFORMATION:
; APPLICANT: LEHRER, ROBERT I.
; APPLICANT: HARMIG, SYLVIA S.L.
; APPLICANT: KORYAKOV, VLADIMIR N.
; TITLE OF INVENTION: PROTEGRINS
; NUMBER OF SEQUENCES: 76
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: PENNIE & EDMONDS LLP
; STREET: 1155 Avenue of the Americas
; CITY: New York
; STATE: New York
; COUNTRY: USA
; ZIP: 10036-2711
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/539,443
; FILING DATE: 30-MARCH-2000
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US/09/128,345
; FILING DATE: 03-AUG-1998
; ATTORNEY/AGENT INFORMATION:
; NAME: Coruzzi, Laura, A.

```

```

; REGISTRATION NUMBER: 30,742
; REFERENCE/DOCKET NUMBER: 8067-0054-999
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (212) 790-9090
; TELEFAX: (212) 869-9741
; TELEX: 66141 PENNIE
; INFORMATION FOR SEQ ID NO: 54:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 18 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; FEATURE:
; NAME/KEY: Disulfide-bond
; LOCATION: 8..13
; FEATURES:
; NAME/KEY: Modified-eite
; LOCATION: group(6, 15)
; OTHER INFORMATION: /note= "X is a hydrophobic, a
; OTHER INFORMATION: small, or a large polar amino acid"
;
US-09-539-443-54

```

```

Query Match 68.1%; Score 62; DB 3; Length 18;
Best Local Similarity 66.7%; Pred. No. 0.0086;
Matches 12; Conservative 0; Mismatches 6; Indels 0; Gaps 0;

```

```

Qy 1 RGGRLSYRRRPFSTGCR 18
    ||||| ||||| ||
Db 1 RGGRLCYRRRFXVCVGR 18

```

```

RESULT 26
US-09-539-443-59
; Sequence 59, Application US/09539443
; Publication No. US20030100483A1
; GENERAL INFORMATION:
; APPLICANT: LEHRER, ROBERT I.
; APPLICANT: HARMIG, SYLVIA S.L.
; APPLICANT: KORYAKOV, VLADIMIR N.
; TITLE OF INVENTION: PROTEGRINS
; NUMBER OF SEQUENCES: 76
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: PENNIE & EDMONDS LLP
; STREET: 1155 Avenue of the Americas
; CITY: New York
; STATE: New York
; COUNTRY: USA
; ZIP: 10036-2711
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/539,443
; FILING DATE: 30-MARCH-2000
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US/09/128,345
; FILING DATE: 03-AUG-1998
; ATTORNEY/AGENT INFORMATION:
; NAME: Coruzzi, Laura, A.
; REGISTRATION NUMBER: 30,742
; REFERENCE/DOCKET NUMBER: 8067-0054-999
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (212) 790-9090
; TELEFAX: (212) 869-9741
; TELEX: 66141 PENNIE
; INFORMATION FOR SEQ ID NO: 59:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 18 amino acids
; TYPE: amino acid
; STRANDEDNESS: single

```

; TOPOLOGY: linear  
 ; FEATURE:  
 ; NAME/KEY: Disulfide-bond  
 ; LOCATION: 6..15  
 ; FEATURE:  
 ; NAME/KEY: Modified-site  
 ; LOCATION: group(8, 13)  
 ; OTHER INFORMATION: /note= "X is a hydrophobic, a  
 ; OTHER INFORMATION: small, or a large polar amino acid"  
 ; US-09-539-443-59

Query Match 68.1%; Score 62; DB 3; Length 18;  
 Best Local Similarity 66.7%; Pred. No. 0.0089;  
 Matches 12; Conservative 0; Mismatches 6; Indels 0; Gaps 0;

QY 1 RGRGLYSRRRFRSTGTGR 18  
 ||||| ||||| |||||  
 Db 1 RGRGLCYXRRRFXICVGR 18

RESULT 27  
 US-10-627-829-54  
 ; Sequence 54, Application US/10627829  
 ; Publication No. US20040152638A1  
 ; GENERAL INFORMATION:  
 ; APPLICANT: LEHRER, ROBERT I.  
 ; APPLICANT: HARWIG, SYLVIA S.L.  
 ; APPLICANT: KOKRYAKOV, VLADIMIR N.  
 ; TITLE OF INVENTION: PROTEGRINS  
 ; NUMBER OF SEQUENCES: 76  
 ; CORRESPONDENCE ADDRESS:  
 ; ADDRESSEE: PENNIE & EDMONDS LLP  
 ; STREET: 1155 Avenue of the Americas  
 ; CITY: New York  
 ; STATE: New York  
 ; COUNTRY: USA  
 ; ZIP: 10036-2711  
 ; COMPUTER READABLE FORM:  
 ; MEDIUM TYPE: Floppy disk  
 ; COMPUTER: IBM PC compatible  
 ; OPERATING SYSTEM: PC-DOS/MS-DOS  
 ; SOFTWARE: PatentIn Release #1.0, Version #1.30  
 ; CURRENT APPLICATION DATA:  
 ; APPLICATION NUMBER: US/10/627,829  
 ; FILING DATE: 24-JULY-2003  
 ; CLASSIFICATION:  
 ; PRIOR APPLICATION DATA:  
 ; APPLICATION NUMBER: US/09/539,443  
 ; FILING DATE: 30-MARCH-2000  
 ; APPLICATION NUMBER: US/09/128,345  
 ; FILING DATE: 03-AUG-1998  
 ; ATTORNEY/AGENT INFORMATION:  
 ; NAME: Coruzzi, Laura, A.  
 ; REGISTRATION NUMBER: 30,742  
 ; REFERENCE/DOCKET NUMBER: 8067-0054-999  
 ; TELEPHONE: (212) 790-9090  
 ; TELEFAX: (212) 869-9741  
 ; INFORMATION FOR SEQ ID NO: 54:  
 ; REGISTRATION NUMBER: 30,742  
 ; REFERENCE/DOCKET NUMBER: 8067-0054-999  
 ; TELEPHONE: (212) 790-9090  
 ; TELEFAX: (212) 869-9741  
 ; INFORMATION FOR SEQ ID NO: 54:  
 ; REGISTRATION NUMBER: 30,742  
 ; REFERENCE/DOCKET NUMBER: 8067-0054-999  
 ; TELEPHONE: (212) 790-9090  
 ; TELEFAX: (212) 869-9741  
 ; SEQUENCE CHARACTERISTICS:  
 ; LENGTH: 18 amino acids  
 ; TYPE: amino acid  
 ; STRANDEDNESS: single  
 ; TOPOLOGY: linear  
 ; FEATURE:  
 ; NAME/KEY: Disulfide-bond  
 ; LOCATION: 8..13  
 ; FEATURE:  
 ; NAME/KEY: Modified-site  
 ; LOCATION: group(6, 15)  
 ; OTHER INFORMATION: /note= "X is a hydrophobic, a  
 ; OTHER INFORMATION: small, or a large polar amino acid"

US-10-627-829-54  
 Query Match 68.1%; Score 62; DB 4; Length 18;  
 Best Local Similarity 66.7%; Pred. No. 0.0088;  
 Matches 12; Conservative 0; Mismatches 6; Indels 0; Gaps 0;

QY 1 RGRGLYSRRRFRSTGTGR 18  
 ||||| ||||| |||||  
 Db 1 RGRGLCYXRRRFXICVGR 18

RESULT 28  
 US-10-627-829-59  
 ; Sequence 59, Application US/10627829  
 ; Publication No. US20040152638A1  
 ; GENERAL INFORMATION:  
 ; APPLICANT: LEHRER, ROBERT I.  
 ; APPLICANT: HARWIG, SYLVIA S.L.  
 ; APPLICANT: KOKRYAKOV, VLADIMIR N.  
 ; TITLE OF INVENTION: PROTEGRINS  
 ; NUMBER OF SEQUENCES: 76  
 ; CORRESPONDENCE ADDRESS:  
 ; ADDRESSEE: PENNIE & EDMONDS LLP  
 ; STREET: 1155 Avenue of the Americas  
 ; CITY: New York  
 ; STATE: New York  
 ; COUNTRY: USA  
 ; ZIP: 10036-2711  
 ; COMPUTER READABLE FORM:  
 ; MEDIUM TYPE: Floppy disk  
 ; COMPUTER: IBM PC compatible  
 ; OPERATING SYSTEM: PC-DOS/MS-DOS  
 ; SOFTWARE: PatentIn Release #1.0, Version #1.30  
 ; CURRENT APPLICATION DATA:  
 ; APPLICATION NUMBER: US/10/627,829  
 ; FILING DATE: 24-JULY-2003  
 ; CLASSIFICATION:  
 ; PRIOR APPLICATION DATA:  
 ; APPLICATION NUMBER: US/09/539,443  
 ; FILING DATE: 30-MARCH-2000  
 ; APPLICATION NUMBER: US/09/128,345  
 ; FILING DATE: 03-AUG-1998  
 ; ATTORNEY/AGENT INFORMATION:  
 ; NAME: Coruzzi, Laura, A.  
 ; REGISTRATION NUMBER: 30,742  
 ; REFERENCE/DOCKET NUMBER: 8067-0054-999  
 ; TELEPHONE: (212) 790-9090  
 ; TELEFAX: (212) 869-9741  
 ; INFORMATION FOR SEQ ID NO: 59:  
 ; SEQUENCE CHARACTERISTICS:  
 ; LENGTH: 18 amino acids  
 ; TYPE: amino acid  
 ; STRANDEDNESS: single  
 ; TOPOLOGY: linear  
 ; FEATURE:  
 ; NAME/KEY: Disulfide-bond  
 ; LOCATION: 6..15  
 ; FEATURE:  
 ; NAME/KEY: Modified-site  
 ; LOCATION: group(8, 13)  
 ; OTHER INFORMATION: /note= "X is a hydrophobic, a  
 ; OTHER INFORMATION: small, or a large polar amino acid"

Query Match 68.1%; Score 62; DB 4; Length 18;  
 Best Local Similarity 66.7%; Pred. No. 0.0089;  
 Matches 12; Conservative 0; Mismatches 6; Indels 0; Gaps 0;

QY 1 RGRGLYSRRRFRSTGTGR 18  
 ||||| ||||| |||||  
 Db 1 RGRGLCYXRRRFXICVGR 18

## RESULT 29

US-09-030-619-221  
; Sequence 221, Application US/09030619B  
; Patent No. US20020035061A1  
; GENERAL INFORMATION:  
; APPLICANT: Krieger, Timothy J.  
; APPLICANT: Taylor, Robert  
; APPLICANT: Erfile, Douglas  
; APPLICANT: Fraser, Janet R.  
; APPLICANT: West, Michael H.P.  
; APPLICANT: McNicol, Patricia J.  
; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR TREATING  
; TITLE OF INVENTION: INFECTIONS USING CATIONIC PEPTIDES ALONE OR IN COMBINATION  
; FILE REFERENCE: 660081.406  
; CURRENT FILING DATE: 1998-02-25  
; NUMBER OF SEQ ID NOS: 232  
; SOFTWARE: FastSeq for Windows Version 3.0  
; SEQ ID NO 221  
; LENGTH: 18  
; TYPE: PRT  
; ORGANISM: Sus scrofa

US-09-030-619-221

Query Match 67.0%; Score 61; DB 3; Length 18;  
Best Local Similarity 66.7%; Pred. No. 0.013;  
Matches 12; Conservative 0; Mismatches 6; Indels 0; Gaps 0;

QY 1 RGGRLSYRRRFFSTGTGR 18  
||||| ||||| ||  
Db 1 RGGRLCYRRRFFCVGVR 18

## RESULT 30

US-09-912-609-109  
; Sequence 109, Application US/09912609  
; Publication No. US20020041898A1  
; GENERAL INFORMATION:  
; APPLICANT: UNGER, EVAN C.  
; APPLICANT: MATSUNAGA, TERRY ONICHI  
; APPLICANT: RAMASWAMI, VARADARAJAN  
; APPLICANT: ROMANOWSKI, MAREK J.  
; TITLE OF INVENTION: NOVEL TARGETED DELIVERY SYSTEMS FOR BIOACTIVE AGENTS  
; FILE REFERENCE: 5030-0001.24  
; CURRENT APPLICATION NUMBER: US/09/912,609  
; CURRENT FILING DATE: 2001-07-25  
; PRIOR APPLICATION NUMBER: 09/703,474  
; PRIOR FILING DATE: 2000-10-31  
; PRIOR APPLICATION NUMBER: 09/478,124  
; PRIOR FILING DATE: 2000-01-05  
; NUMBER OF SEQ ID NOS: 131  
; SOFTWARE: PatentIn Ver. 2.1  
; SEQ ID NO 109  
; LENGTH: 18  
; TYPE: PRT  
; ORGANISM: Artificial Sequence  
; FEATURE:  
; OTHER INFORMATION: Description of Artificial Sequence: Synthetic  
; OTHER INFORMATION: peptide

US-09-912-609-109

Query Match 67.0%; Score 61; DB 3; Length 18;  
Best Local Similarity 66.7%; Pred. No. 0.013;  
Matches 12; Conservative 0; Mismatches 6; Indels 0; Gaps 0;

QY 1 RGGRLSYRRRFFSTGTGR 18  
||||| ||||| ||  
Db 1 RGGRLCYRRRFFCVGVR 18

## RESULT 31

US-09-539-443-11  
; Sequence 11, Application US/09539443  
; Publication No. US20030100483A1  
; GENERAL INFORMATION:  
; APPLICANT: LEHRER, ROBERT I.  
; APPLICANT: HARWIG, SYLVIA S.L.  
; APPLICANT: KORYAKOV, VLADIMIR N.  
; TITLE OF INVENTION: PROTEGRINS  
; NUMBER OF SEQUENCES: 76  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: PENNIE & EDMONDS LLP  
; STREET: 1155 Avenue of the Americas  
; CITY: New York  
; STATE: New York  
; COUNTRY: USA  
; ZIP: 10036-2711  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Floppy disk  
; COMPUTER: IBM PC compatible  
; OPERATING SYSTEM: PC-DOS/MS-DOS  
; SOFTWARE: PatentIn Release #1.0, Version #1.30  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/09/539,443  
; FILING DATE: 30-MARCH-2000  
; CLASSIFICATION:  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: US/09/128,345  
; FILING DATE: 03-AUG-1998  
; ATTORNEY/AGENT INFORMATION:  
; NAME: Coruzzi, Laura, A.  
; REGISTRATION NUMBER: 30,742  
; REFERENCE/DOCKET NUMBER: 8067-0054-999  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: (212) 790-9090  
; TELEFAX: (212) 869-9741  
; TELEX: 66141 PENNIE  
; INFORMATION FOR SEQ ID NO: 11:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 18 amino acids  
; TYPE: amino acid  
; STRANDEDNESS: single  
; TOPOLOGY: linear  
; FEATURE:  
; NAME/KEY: Disulfide-bond  
; LOCATION: 4..13  
; FEATURE:  
; NAME/KEY: Disulfide-bond  
; LOCATION: 6..11  
; US-09-539-443-11

Query Match 67.0%; Score 61; DB 3; Length 18;  
Best Local Similarity 66.7%; Pred. No. 0.013;  
Matches 12; Conservative 0; Mismatches 6; Indels 0; Gaps 0;

QY 1 RGGRLSYRRRFFSTGTGR 18  
||||| ||||| ||  
Db 1 RGGRLCYRRRFFCVGVR 18

## RESULT 32

US-09-539-443-16  
; Sequence 16, Application US/09539443  
; Publication No. US20030100483A1  
; GENERAL INFORMATION:  
; APPLICANT: LEHRER, ROBERT I.  
; APPLICANT: HARWIG, SYLVIA S.L.  
; APPLICANT: KORYAKOV, VLADIMIR N.  
; TITLE OF INVENTION: PROTEGRINS  
; NUMBER OF SEQUENCES: 76  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: PENNIE & EDMONDS LLP  
; STREET: 1155 Avenue of the Americas

CITY: New York  
STATE: New York  
COUNTRY: USA  
ZIP: 10036-2711  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: Patent In Release #1.0, Version #1.30  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/09/539,443  
FILING DATE: 30-MARCH-2000  
CLASSIFICATION:  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US/09/128,345  
FILING DATE: 03-AUG-1998  
ATTORNEY/AGENT INFORMATION:  
NAME: Coruzzi, Laura, A.  
REGISTRATION NUMBER: 30,742  
REFERENCE/DOCKET NUMBER: 8067-0054-999  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (212) 790-9090  
TELEFAX: (212) 869-9741  
TELEX: 66141 PENNIE  
INFORMATION FOR SEQ ID NO: 16:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 18 amino acids  
TYPE: amino acid  
STRANDEDNESS: single  
TOPOLOGY: linear  
US-09-539-443-16

Query Match 67.0%; Score 61; DB 3; Length 18;  
Best Local Similarity 66.7%; Pred. No. 0.013;  
Matches 12; Conservative 0; Mismatches 6; Indels 0; Gaps 0;

QY 1 RGRLSYSRRRSTSTGR 18  
Db 1 RGRLCYCRRRFCVCVGR 18

RESULT 33  
US-09-539-443-33  
Sequence 33, Application US/09539443  
Publication No. US20030100483A1  
GENERAL INFORMATION:  
APPLICANT: LEHRER, ROBERT I.  
APPLICANT: HARWIG, SYLVIA S.L.  
APPLICANT: KOKRYAKOV, VLADIMIR N.  
TITLE OF INVENTION: PROTEGRINS  
NUMBER OF SEQUENCES: 76  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: PENNIE & EDMONDS LLP  
STREET: 1155 Avenue of the Americas  
CITY: New York  
STATE: New York  
COUNTRY: USA  
ZIP: 10036-2711  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: Patent In Release #1.0, Version #1.30  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/09/539,443  
FILING DATE: 30-MARCH-2000  
CLASSIFICATION:  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US/09/128,345  
FILING DATE: 03-AUG-1998  
ATTORNEY/AGENT INFORMATION:  
NAME: Coruzzi, Laura, A.  
REGISTRATION NUMBER: 30,742

REFERENCE/DOCKET NUMBER: 8067-0054-999  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (212) 790-9090  
TELEFAX: (212) 869-9741  
TELEX: 66141 PENNIE  
INFORMATION FOR SEQ ID NO: 33:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 18 amino acids  
TYPE: amino acid  
STRANDEDNESS: single  
TOPOLOGY: linear  
FEATURE:  
NAME/KEY: Region  
LOCATION: 1..18  
OTHER INFORMATION: /note= "All D-form amino acids"  
US-09-539-443-33

Query Match 67.0%; Score 61; DB 3; Length 18;  
Best Local Similarity 66.7%; Pred. No. 0.013;  
Matches 12; Conservative 0; Mismatches 6; Indels 0; Gaps 0;

QY 1 RGRLSYSRRRSTSTGR 18  
Db 1 RGRLCYCRRRFCVCVGR 18

RESULT 34  
US-09-539-443-48  
Sequence 48, Application US/09539443  
Publication No. US20030100483A1  
GENERAL INFORMATION:  
APPLICANT: LEHRER, ROBERT I.  
APPLICANT: HARWIG, SYLVIA S.L.  
APPLICANT: KOKRYAKOV, VLADIMIR N.  
TITLE OF INVENTION: PROTEGRINS  
NUMBER OF SEQUENCES: 76  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: PENNIE & EDMONDS LLP  
STREET: 1155 Avenue of the Americas  
CITY: New York  
STATE: New York  
COUNTRY: USA  
ZIP: 10036-2711  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: Patent In Release #1.0, Version #1.30  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/09/539,443  
FILING DATE: 30-MARCH-2000  
CLASSIFICATION:  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US/09/128,345  
FILING DATE: 03-AUG-1998  
ATTORNEY/AGENT INFORMATION:  
NAME: Coruzzi, Laura, A.  
REGISTRATION NUMBER: 30,742  
REFERENCE/DOCKET NUMBER: 8067-0054-999  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (212) 790-9090  
TELEFAX: (212) 869-9741  
TELEX: 66141 PENNIE  
INFORMATION FOR SEQ ID NO: 48:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 18 amino acids  
TYPE: amino acid  
STRANDEDNESS: single  
TOPOLOGY: linear  
US-09-539-443-48

Query Match 67.0%; Score 61; DB 3; Length 18;  
Best Local Similarity 66.7%; Pred. No. 0.013;

Matches 12; Conservative 2; Mismatches 4; Indels 0; Gaps 0;

Qy 1 RGGRLSYRRRFFSTSTGR 18  
| : | | | | | | | |  
Db 1 RATRISFRRRFSVSVGR 18

## RESULT 35

US-10-077-624-15  
; Sequence 15, Application US/10077624  
; Publication No. US20030143234A1  
; GENERAL INFORMATION:  
; APPLICANT: THE REGENTS OF THE UNIVERSITY OF CALIFORNIA  
; APPLICANT: WASHINGTON DENTAL SERVICE  
; APPLICANT: Shi, Wenyuan  
; APPLICANT: Anderson, Maxwell  
; APPLICANT: Morrison, Sherie  
; APPLICANT: Trinh, Kham  
; APPLICANT: Wims, Letitia  
; APPLICANT: Chen, Li  
; APPLICANT: Qi, Fengxia  
; TITLE OF INVENTION: ANTI-MICROBIAL TARGETING CHIMERIC PHARMACEUTICAL  
; FILE REFERENCE: 2101363-991200  
; CURRENT APPLICATION NUMBER: US/10/077,624  
; CURRENT FILING DATE: 2002-02-14  
; PRIOR FILING DATE: US 09/910,358  
; PRIOR FILING DATE: 2001-07-19  
; PRIOR FILING DATE: US 09/378,577  
; PRIOR FILING DATE: 1999-08-20  
; NUMBER OF SEQ ID NOS: 31  
; SOFTWARE: PatentIn version 3.1  
; SEQ ID NO 15  
; LENGTH: 18  
; TYPE: PRT  
; ORGANISM: Artificial sequence  
; FEATURE:  
; OTHER INFORMATION: Protegrin PG-1  
US-10-077-624-15

Query Match 67.0%; Score 61; DB 4; Length 18;  
Best Local Similarity 66.7%; Pred. No. 0.013; Mismatches 6; Indels 0; Gaps 0;  
Matches 12; Conservative 0; Mismatches 6; Indels 0; Gaps 0;

Qy 1 RGGRLSYRRRFFSTSTGR 18  
| | | | | | | | | |  
Db 1 RGGRLCYRRRFFCVGVR 18

## RESULT 36

US-10-313-994-11  
; Sequence 11, Application US/10313994  
; Publication No. US20030162718A1  
; GENERAL INFORMATION:  
; APPLICANT: Selssted, Michael E.  
; APPLICANT: Tang, Yi-Quan  
; APPLICANT: Yuan, Jun  
; TITLE OF INVENTION: Antimicrobial Theta Defensins and Methods of Using Same  
; FILE REFERENCE: P-UC 3095  
; CURRENT APPLICATION NUMBER: US/10/313,994  
; CURRENT FILING DATE: 2002-12-05  
; PRIOR FILING DATE: US/09/309,487  
; PRIOR FILING DATE: 1999-05-10  
; NUMBER OF SEQ ID NOS: 31  
; SOFTWARE: PatentIn Ver. 2.0  
; SEQ ID NO 11  
; LENGTH: 18  
; TYPE: PRT  
; ORGANISM: Sus scrofa  
US-10-313-994-11

Query Match 67.0%; Score 61; DB 4; Length 18;  
Best Local Similarity 66.7%; Pred. No. 0.013; Mismatches 6; Indels 0; Gaps 0;

Matches 12; Conservative 0; Mismatches 6; Indels 0; Gaps 0;

Qy 1 RGGRLSYRRRFFSTSTGR 18  
| | | | | | | | | |  
Db 1 RGGRLCYRRRFFCVGVR 18

## RESULT 37

US-10-277-232-221  
; Sequence 221, Application US/10277232  
; Publication No. US20030211537A1  
; GENERAL INFORMATION:  
; APPLICANT: Krieger, Timothy J.  
; APPLICANT: Taylor, Robert  
; APPLICANT: Exfile, Douglas  
; APPLICANT: Fraser, Janet R.  
; APPLICANT: West, Michael H.P.  
; APPLICANT: McNicol, Patricia J.  
; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR TREATING  
; TITLE OF INVENTION: INFECTIONS USING CATIONIC PEPTIDES ALONE OR IN COMBINATION  
; FILE REFERENCE: 660081.406C1  
; CURRENT APPLICATION NUMBER: US/10/277,232  
; CURRENT FILING DATE: 2002-11-27  
; NUMBER OF SEQ ID NOS: 232  
; SOFTWARE: FastSeq for Windows Version 3.0  
; SEQ ID NO 221  
; LENGTH: 18  
; TYPE: PRT  
; ORGANISM: Sus scrofa  
US-10-277-232-221

Query Match 67.0%; Score 61; DB 4; Length 18;  
Best Local Similarity 66.7%; Pred. No. 0.013; Mismatches 6; Indels 0; Gaps 0;  
Matches 12; Conservative 0; Mismatches 6; Indels 0; Gaps 0;

Qy 1 RGGRLSYRRRFFSTSTGR 18  
| | | | | | | | | |  
Db 1 RGGRLCYRRRFFCVGVR 18

## RESULT 38

US-10-277-233-221  
; Sequence 221, Application US/10277233  
; Publication No. US20030232750A1  
; GENERAL INFORMATION:  
; APPLICANT: Krieger, Timothy J.  
; APPLICANT: Taylor, Robert  
; APPLICANT: Exfile, Douglas  
; APPLICANT: Fraser, Janet R.  
; APPLICANT: West, Michael H.P.  
; APPLICANT: McNicol, Patricia J.  
; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR TREATING  
; TITLE OF INVENTION: INFECTIONS USING CATIONIC PEPTIDES ALONE OR IN COMBINATION  
; FILE REFERENCE: 660081.406C1  
; CURRENT APPLICATION NUMBER: US/10/277,233  
; CURRENT FILING DATE: 2002-10-18  
; NUMBER OF SEQ ID NOS: 232  
; SOFTWARE: FastSeq for Windows Version 3.0  
; SEQ ID NO 221  
; LENGTH: 18  
; TYPE: PRT  
; ORGANISM: Sus scrofa  
US-10-277-233-221

Query Match 67.0%; Score 61; DB 4; Length 18;  
Best Local Similarity 66.7%; Pred. No. 0.013; Mismatches 6; Indels 0; Gaps 0;  
Matches 12; Conservative 0; Mismatches 6; Indels 0; Gaps 0;

Qy 1 RGGRLSYRRRFFSTSTGR 18  
| | | | | | | | | |  
Db 1 RGGRLCYRRRFFCVGVR 18

Job time : 182 secs

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RESULT 39
US-10-427-715-32
; Sequence 32, Application US/10427715
; Publication No. US20040014669A1
; GENERAL INFORMATION:
; APPLICANT: Selsted, Michael E.
; APPLICANT: Tran, Dat Q.
; TITLE OF INVENTION: Antimicrobial Theta Defensins, Analogs
; TITLE OF INVENTION: Thereof, and Methods of Use
; FILE REFERENCE: 66778-302(UC5754)
; CURRENT APPLICATION NUMBER: US/10/427,715
; CURRENT FILING DATE: 2003-04-30
; PRIOR APPLICATION NUMBER: US 60/377,071
; PRIOR FILING DATE: 2002-04-30
; NUMBER OF SEQ ID NOS: 41
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 32
; LENGTH: 18
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: synthetic construct
; NAME/KEY: AMIDATION
; LOCATION: 18
; OTHER INFORMATION: at the C terminus
US-10-427-715-32

```

```

Query Match      67.0%; Score 61; DB 4; Length 18;
Best Local Similarity 66.7%; Pred. No. 0.013;
Matches 12; Conservative 0; Mismatches 6; Indels 0; Gaps 0;

QY      1 RGGRLSYRRRRFSTGTGR 18
        ||||| ||||| ||
Db       1 RGGRLCYCRRRFCVCVGR 18

```

```

RESULT 40
US-10-427-715-33
; Sequence 33, Application US/10427715
; Publication No. US20040014669A1
; GENERAL INFORMATION:
; APPLICANT: Selsted, Michael E.
; APPLICANT: Tran, Dat Q.
; TITLE OF INVENTION: Antimicrobial Theta Defensins, Analogs
; TITLE OF INVENTION: Thereof, and Methods of Use
; FILE REFERENCE: 66778-302(UC5754)
; CURRENT APPLICATION NUMBER: US/10/427,715
; CURRENT FILING DATE: 2003-04-30
; PRIOR APPLICATION NUMBER: US 60/377,071
; PRIOR FILING DATE: 2002-04-30
; NUMBER OF SEQ ID NOS: 41
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 33
; LENGTH: 18
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: synthetic construct
US-10-427-715-33

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```

Query Match      67.0%; Score 61; DB 4; Length 18;
Best Local Similarity 66.7%; Pred. No. 0.013;
Matches 12; Conservative 0; Mismatches 6; Indels 0; Gaps 0;

QY      1 RGGRLSYRRRRFSTGTGR 18
        ||||| ||||| ||
Db       1 RGGRLCYCRRRFCVCVGR 18

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Search completed: May 21, 2006, 00:39:20

GenCore version 5.1.8  
Copyright (c) 1993 - 2006 Bioceleration Ltd.

OM protein - protein search, using sw model

Run on: May 21, 2006, 00:36:21 ; Search time 9 Seconds  
(without alignments)  
4.272 Million cell updates/sec

Title: US-09-857-000a-11

Perfect score: 91

Sequence: 1 RGRLSYRRRRFSTSTGR 18

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 21570 seqs, 2136119 residues

Total number of hits satisfying chosen parameters: 21570

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 100 summaries

Database : Published Applications AA New:\*

- 1: /EMC\_Ce1erra\_SIDS3/ptodata/2/pubpaa/US09\_NEW\_PUB.pbp.\*
- 2: /EMC\_Ce1erra\_SIDS3/ptodata/2/pubpaa/US06\_NEW\_PUB.pbp.\*
- 3: /EMC\_Ce1erra\_SIDS3/ptodata/2/pubpaa/US07\_NEW\_PUB.pbp.\*
- 4: /EMC\_Ce1erra\_SIDS3/ptodata/2/pubpaa/US08\_NEW\_PUB.pbp.\*
- 5: /EMC\_Ce1erra\_SIDS3/ptodata/2/pubpaa/PCT\_NEW\_PUB.pbp.\*
- 6: /EMC\_Ce1erra\_SIDS3/ptodata/2/pubpaa/US10\_NEW\_PUB.pbp.\*
- 7: /EMC\_Ce1erra\_SIDS3/ptodata/2/pubpaa/US11\_NEW\_PUB.pbp.\*
- 8: /EMC\_Ce1erra\_SIDS3/ptodata/2/pubpaa/US60\_NEW\_PUB.pbp.\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	37	40.7	413	7	US-11-249-111-87
2	34.5	37.9	390	7	US-11-242-505A-27
3	34	37.4	421	6	US-10-505-928-410
4	34	37.4	967	6	US-10-505-928-795
5	33.5	36.8	4059	6	US-10-501-834-6
6	33	36.3	525	6	US-10-196-749-436
7	32	35.2	95	7	US-11-239-308-40
8	32	35.2	226	6	US-10-505-928-193
9	32	35.2	302	7	US-11-058-746-9
10	32	35.2	352	7	US-11-242-505A-6
11	32	35.2	362	6	US-10-511-937-2509
12	32	35.2	372	7	US-11-058-746-10
13	32	35.2	383	7	US-11-058-746-6
14	32	35.2	384	7	US-11-058-746-7
15	32	35.2	640	7	US-11-249-111-96
16	32	35.2	3256	6	US-10-505-928-357
17	31	34.1	180	6	US-10-505-928-648
18	31	34.1	235	7	US-11-266-747-434
19	31	34.1	551	7	US-11-264-784-34
20	31	34.1	708	6	US-10-505-928-416
21	31	34.1	747	7	US-11-261-384-2
22	31	34.1	901	6	US-10-511-455-52
23	31	34.1	938	6	US-10-511-455-54
24	31	34.1	950	6	US-10-511-937-2603
25	31	34.1	1924	6	US-10-512-386-56

Sequence 7, Appli  
Sequence 3, Appli  
Sequence 131, App  
Sequence 132, App  
Sequence 133, App  
Sequence 175, App  
Sequence 176, App  
Sequence 177, App  
Sequence 178, App  
Sequence 179, App  
Sequence 24, Appl  
Sequence 16, Appl  
Sequence 2, Appli  
Sequence 2466, Ap  
Sequence 2608, Ap  
Sequence 2530, Ap  
Sequence 845, App  
Sequence 6, Appli  
Sequence 389, App  
Sequence 6, Appli  
Sequence 4, Appli  
Sequence 2, Appli  
Sequence 2, Appli  
Sequence 2421, Ap  
Sequence 13, Appl  
Sequence 7, Appli  
Sequence 17, Appl  
Sequence 171, App  
Sequence 124, App  
Sequence 125, App  
Sequence 173, App  
Sequence 2, Appli  
Sequence 4, Appli  
Sequence 6, Appli  
Sequence 10, Appl  
Sequence 12, Appl  
Sequence 121, App  
Sequence 122, App  
Sequence 123, App  
Sequence 126, App  
Sequence 127, App  
Sequence 167, App  
Sequence 168, App  
Sequence 169, App  
Sequence 170, App  
Sequence 172, App  
Sequence 784, App  
Sequence 1, Appli  
Sequence 8, Appli  
Sequence 12, Appl  
Sequence 57, Appl  
Sequence 2549, Ap  
Sequence 514, App  
Sequence 457, App  
Sequence 757, App  
Sequence 14, Appl  
Sequence 154, App  
Sequence 3, Appli  
Sequence 3007, Ap  
Sequence 364, App  
Sequence 43, Appl  
Sequence 769, App  
Sequence 770, App  
Sequence 772, App  
Sequence 68, Appl  
Sequence 436, App  
Sequence 536, App  
Sequence 2469, Ap  
Sequence 67, Appl  
Sequence 7, Appl  
Sequence 2, Appli  
Sequence 4, Appli  
Sequence 33, Appl

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99      28 30.8 653 7 US-11-183-218-66      Sequence 66, Appl
100     28 30.8 694 6 US-10-505-928-312      Sequence 312, App

ALIGNMENTS

RESULT 1
US-11-249-111-87
; Sequence 87, Application US/11249111
; Publication No. US20060099623A1
; GENERAL INFORMATION:
; APPLICANT: Glenn, Matthew
; APPLICANT: Lubbers, Mark W
; APPLICANT: Dekker, James
; TITLE OF INVENTION: Polynucleotides and polypeptides isolated from Lactobacillus
; FILE OF INVENTION: and methods for their use.
; FILE REFERENCE: 13353.1048ulc2
; CURRENT APPLICATION NUMBER: US/11/249,111
; CURRENT FILING DATE: 2005-10-11
; PRIOR APPLICATION NUMBER: 10/288,930
; PRIOR FILING DATE: 2002-11-05
; PRIOR APPLICATION NUMBER: 09/724,623
; PRIOR FILING DATE: 2000-11-28
; PRIOR APPLICATION NUMBER: 60/148,801
; PRIOR FILING DATE: 1999-12-02
; NUMBER OF SEQ ID NOS: 124
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 87
; LENGTH: 413
; TYPE: PRT
; ORGANISM: Lactobacillus rhamnosus
US-11-249-111-87

Query Match      40.7%; Score 37; DB 7; Length 413;
Best Local Similarity 42.9%; Pred. No. 7.2;
Matches 6; Conservative 4; Mismatches 4; Indels 0; Gaps 0;

QY      5 LSYRRRRFSTSTGR 18
DB      88 LSYKRRKITTAVGK 101

RESULT 2
US-11-242-505A-27
; Sequence 27, Application US/11242505A
; Publication No. US20060099656A1
; GENERAL INFORMATION:
; APPLICANT: Carroll, Joseph M.
; APPLICANT: Healy, Aileen
; TITLE OF INVENTION: Methods and Compositions for Treating
; FILE OF INVENTION: Hematological Disorders Using 232, 2059, 10630, 12848, 13875,
; FILE REFERENCE: 14395, 14618, 17692, 58874, 252, 304, 1980, 14717, 9941, 19310,
; CURRENT APPLICATION NUMBER: US/11/242,505A
; CURRENT FILING DATE: 2005-10-03
; PRIOR APPLICATION NUMBER: US 10/290,078
; PRIOR FILING DATE: 2002-11-07
; PRIOR APPLICATION NUMBER: US 60/347,949
; PRIOR FILING DATE: 2001-11-07
; PRIOR APPLICATION NUMBER: US 10/320,351
; PRIOR FILING DATE: 2002-12-16
; PRIOR APPLICATION NUMBER: 60/341,606
; PRIOR FILING DATE: 2001-12-17
; NUMBER OF SEQ ID NOS: 48
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 27
; LENGTH: 390
; TYPE: PRT
; ORGANISM: Homo Sapiens
US-11-242-505A-27

Query Match      37.9%; Score 34.5; DB 7; Length 390;

US-09-857-000a-11.rapbn
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Best Local Similarity 71.4%; Pred. No. 20;
Matches 10; Conservative 0; Mismatches 3; Indels 1; Gaps 1;

QY      3 GRLSYRRRPFSTST 16
DB      230 GRLS-SRRSLAST 242

RESULT 3
US-10-505-928-410
; Sequence 410, Application US/10505928
; Publication No. US20060088532A1
; GENERAL INFORMATION:
; APPLICANT: Ludwig Institute for Cancer Research et al.
; TITLE OF INVENTION: LYMPHATIC ENDOTHELIAL GENES
; FILE REFERENCE: 28967/39178
; CURRENT APPLICATION NUMBER: US/10/505,928
; CURRENT FILING DATE: 2004-08-27
; PRIOR APPLICATION NUMBER: US 60/363,019
; PRIOR FILING DATE: 2002-03-07
; NUMBER OF SEQ ID NOS: 866
; SOFTWARE: PatentIn 3.2
; SEQ ID NO 410
; LENGTH: 421
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-505-928-410

Query Match      37.4%; Score 34; DB 6; Length 421;
Best Local Similarity 40.0%; Pred. No. 27;
Matches 6; Conservative 3; Mismatches 6; Indels 0; Gaps 0;

QY      4 RLSYSRRRPFSTSTGR 18
DB      334 RMSYQRAWEVDSDGR 348

RESULT 4
US-10-505-928-795
; Sequence 795, Application US/10505928
; Publication No. US20060088532A1
; GENERAL INFORMATION:
; APPLICANT: Ludwig Institute for Cancer Research et al.
; TITLE OF INVENTION: LYMPHATIC ENDOTHELIAL GENES
; FILE REFERENCE: 28967/39178
; CURRENT APPLICATION NUMBER: US/10/505,928
; CURRENT FILING DATE: 2004-08-27
; PRIOR APPLICATION NUMBER: US 60/363,019
; PRIOR FILING DATE: 2002-03-07
; NUMBER OF SEQ ID NOS: 866
; SOFTWARE: PatentIn 3.2
; SEQ ID NO 795
; LENGTH: 967
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-505-928-795

Query Match      37.4%; Score 34; DB 6; Length 967;
Best Local Similarity 47.4%; Pred. No. 69;
Matches 9; Conservative 1; Mismatches 3; Indels 6; Gaps 1;

QY      2 GGRLSYSR-----RRFST 14
DB      893 GGSFSSNLIQAVTRRFST 911

RESULT 5
US-10-501-834-6
; Sequence 6, Application US/10501834
; Publication No. US20060088628A1
; GENERAL INFORMATION:
; APPLICANT: Harris, Peter C., Ward, Christopher J., Rossetti, Sandro, and Torres,
; APPLICANT: Vicente E.
```



; TITLE OF INVENTION: Polycystic Kidney Disease Nucleic Acids  
; FILE REFERENCE: 07039/386U1  
; CURRENT APPLICATION NUMBER: US/10/501.834  
; PRIOR FILING DATE: 2004-07-19  
; PRIOR APPLICATION NUMBER: PCT/US03/02038  
; PRIOR FILING DATE: 2003-01-23  
; PRIOR APPLICATION NUMBER: 60/351,110  
; PRIOR FILING DATE: 2002-01-23  
; NUMBER OF SEQ ID NOS: 221  
; SOFTWARE: FastSeq for Windows Version 4.0  
; SEQ ID NO 6  
; LENGTH: 4059  
; TYPE: PRT  
; ORGANISM: Mus musculus  
; FEATURE:  
; NAME/KEY: VARIANT  
; LOCATION: 2511  
; OTHER INFORMATION: Xaa = Pro or Ser  
; FEATURE:  
; NAME/KEY: VARIANT  
; LOCATION: 2981  
; OTHER INFORMATION: Arg or Gln  
US-10-501-834-6

Query Match 36.8%; Score 33.5; DB 6; Length 4059;  
Best Local Similarity 62.5%; Pred. No. 4.4e+02;  
Matches 10; Conservative 0; Mismatches 3; Indels 3; Gaps 1;

Qy 6 SYSRREFSTSTG 18  
||| ||||| |||

Db 2266 SYLDGRFSTSTVGR 2281

## RESULT 6

US-10-196-749-436  
; Sequence 436, Application US/10196749  
; Publication No. US20060094864A1  
; GENERAL INFORMATION:  
; APPLICANT: Baker, Kevin P.  
; APPLICANT: Chen, Jian  
; APPLICANT: Desnoyers, Luc  
; APPLICANT: Goddard, Audrey  
; APPLICANT: Godowski, Paul J.  
; APPLICANT: Gurney, Austin L.  
; APPLICANT: Pan, James  
; APPLICANT: Smith, Victoria  
; APPLICANT: Watanabe, Colin K.  
; APPLICANT: Wood, William I.  
; APPLICANT: Zhang, Zemin  
; TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC  
; FILE REFERENCE: P3430R1C340  
; CURRENT APPLICATION NUMBER: US/10/196,749  
; CURRENT FILING DATE: 2002-07-16  
; PRIOR APPLICATION NUMBER: 10/052586  
; PRIOR FILING DATE: 2002-01-15  
; PRIOR APPLICATION NUMBER: 60/059263  
; PRIOR FILING DATE: 1997-09-18  
; PRIOR APPLICATION NUMBER: 60/059266  
; PRIOR FILING DATE: 1997-09-18  
; PRIOR APPLICATION NUMBER: 60/062250  
; PRIOR FILING DATE: 1997-10-17  
; PRIOR APPLICATION NUMBER: 60/063120  
; PRIOR FILING DATE: 1997-10-24  
; PRIOR APPLICATION NUMBER: 60/063121  
; PRIOR FILING DATE: 1997-10-24  
; PRIOR APPLICATION NUMBER: 60/063486  
; PRIOR FILING DATE: 1997-10-21  
; PRIOR APPLICATION NUMBER: 60/063540  
; PRIOR FILING DATE: 1997-10-28  
; PRIOR APPLICATION NUMBER: 60/063541  
; PRIOR FILING DATE: 1997-10-28

; PRIOR APPLICATION NUMBER: 60/063544  
; PRIOR FILING DATE: 1997-10-28  
; Prior Application data removed - See File Wrapper or PALM.  
; NUMBER OF SEQ ID NOS: 612  
; SEQ ID NO 436  
; LENGTH: 525  
; TYPE: PRT  
; ORGANISM: Homo Sapien  
US-10-196-749-436

Query Match 36.3%; Score 33; DB 6; Length 525;  
Best Local Similarity 57.1%; Pred. No. 52;  
Matches 8; Conservative 1; Mismatches 5; Indels 0; Gaps 0;

Qy 2 GGRLSYRRRFFST 15  
||| ||||| |||  
Db 50 GGGASYSLRRCLSS 63

## RESULT 7

US-11-239-308-40  
; Sequence 40, Application US/11239308  
; Publication No. US2006008883A1  
; GENERAL INFORMATION:  
; APPLICANT: Smider, Vaughn  
; APPLICANT: Larrick, James W.  
; APPLICANT: Integrigen, Inc.  
; TITLE OF INVENTION: Recombinant Catalytic Polypeptides and Their Uses  
; FILE REFERENCE: 021216-000310US  
; CURRENT APPLICATION NUMBER: US/11/239,308  
; CURRENT FILING DATE: 2005-09-28  
; PRIOR APPLICATION NUMBER: US/10/683,733  
; PRIOR FILING DATE: 2003-10-09  
; PRIOR APPLICATION NUMBER: US 60/417,979  
; PRIOR FILING DATE: 2002-10-09  
; NUMBER OF SEQ ID NOS: 62  
; SOFTWARE: PatentIn Ver. 2.1  
; SEQ ID NO 40  
; LENGTH: 95  
; TYPE: PRT  
; ORGANISM: Homo sapiens  
US-11-239-308-40

Query Match 35.2%; Score 32; DB 7; Length 95;  
Best Local Similarity 50.0%; Pred. No. 11;  
Matches 7; Conservative 2; Mismatches 5; Indels 0; Gaps 0;

Qy 4 RLSYRRRFFSTG 17  
|::| |||||  
Db 3 RMTQSPSPFSASTG 16

## RESULT 8

US-10-505-928-193  
; Sequence 193, Application US/10505928  
; Publication No. US20060088532A1  
; GENERAL INFORMATION:  
; APPLICANT: Ludwig Institute for Cancer Research et al.  
; TITLE OF INVENTION: LYMPHATIC ENDOTHELIAL GENES  
; FILE REFERENCE: 28967/39178  
; CURRENT APPLICATION NUMBER: US/10/505,928  
; CURRENT FILING DATE: 2004-08-27  
; PRIOR APPLICATION NUMBER: US 60/363,019  
; PRIOR FILING DATE: 2002-03-07  
; NUMBER OF SEQ ID NOS: 866  
; SOFTWARE: PatentIn 3.2  
; SEQ ID NO 193  
; LENGTH: 226  
; TYPE: PRT  
; ORGANISM: Homo sapiens  
US-10-505-928-193

Query Match 35.2%; Score 32; DB 6; Length 226;

```

Best Local Similarity 44.4%; Pred. No. 30;
Matches 8; Conservative 4; Mismatches 2; Indels 4; Gaps 1;

QY 1 RGGRLSYRRRFFSTSTGR 18
Db 180 RGGPIRFS-----SRSGR 193
|||.:|:|
|||.:|:|

RESULT 9
US-11-058-746-9
; Sequence 9, Application US/11058746
; Publication No. US20060101543A1
; GENERAL INFORMATION:
; APPLICANT: Somerville, Chris
; APPLICANT: Broun, Pierre
; APPLICANT: Van de Loo, Frank
; APPLICANT: Boddupalli, Sekhar S
; TITLE OF INVENTION: PRODUCTION OF HYDROXYLATED FATTY ACIDS IN GENETICALLY MODIFIED
; TITLE OF INVENTION: PLANTS
; FILE REFERENCE: 56100-5022-12
; CURRENT APPLICATION NUMBER: US/11/058,746
; CURRENT FILING DATE: 2005-02-16
; PRIOR APPLICATION NUMBER: US 08/597,313
; PRIOR FILING DATE: 1996-02-06
; PRIOR APPLICATION NUMBER: US 08/530,862
; PRIOR FILING DATE: 1995-09-20
; PRIOR APPLICATION NUMBER: US 08/320,982
; PRIOR FILING DATE: 1994-10-11
; PRIOR APPLICATION NUMBER: US 08/314,596
; PRIOR FILING DATE: 1994-09-26
; PRIOR APPLICATION NUMBER: PCT/US95/11855
; PRIOR FILING DATE: 1995-09-25
; NUMBER OF SEQ ID NOS: 15
; SOFTWARE: PatentIn version 3.3
; SEQ ID NO 9
; LENGTH: 302
; TYPE: PRT
; ORGANISM: Glycine max
US-11-058-746-9

Query Match 35.2%; Score 32; DB 7; Length 302;
Best Local Similarity 54.5%; Pred. No. 42;
Matches 6; Conservative 2; Mismatches 3; Indels 0; Gaps 0;

QY 7 YSRRRFFSTSTG 17
Db 80 YSHRRHHSNTG 90
|||.:|:|
|||.:|:|

RESULT 10
US-11-242-505A-6
; Sequence 6, Application US/11242505A
; Publication No. US20060099656A1
; GENERAL INFORMATION:
; APPLICANT: Carroll, Joseph M.
; APPLICANT: Healy, Aileen
; TITLE OF INVENTION: Methods and Compositions for Treating
; TITLE OF INVENTION: Hematological Disorders Using 232, 2059, 10630, 12848, 13875,
; TITLE OF INVENTION: 14395, 14618, 17692, 58874, 252, 304, 1980, 14717, 9941, 19311
; FILE REFERENCE: MFI2001-288P1RCP10WNIM
; CURRENT APPLICATION NUMBER: US/11/242,505A
; CURRENT FILING DATE: 2005-10-03
; PRIOR APPLICATION NUMBER: US 10/290,078
; PRIOR FILING DATE: 2002-11-07
; PRIOR APPLICATION NUMBER: US 60/347,949
; PRIOR FILING DATE: 2001-11-07
; PRIOR APPLICATION NUMBER: US 10/320,351
; PRIOR FILING DATE: 2002-12-16
; PRIOR APPLICATION NUMBER: 60/341,606
; PRIOR FILING DATE: 2001-12-17
; NUMBER OF SEQ ID NOS: 48
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 6

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; PRIOR APPLICATION NUMBER: US 08/320,982  
; PRIOR FILING DATE: 1994-10-11  
; PRIOR APPLICATION NUMBER: US 08/314,596  
; PRIOR FILING DATE: 1994-09-26  
; PRIOR APPLICATION NUMBER: PCT/US95/11855  
; PRIOR FILING DATE: 1995-09-25  
; NUMBER OF SEQ ID NOS: 15  
; SOFTWARE: PatentIn version 3.3  
; SEQ ID NO 10  
; LENGTH: 372  
; TYPE: PRT  
; ORGANISM: Zea mays  
; FEATURE:  
; NAME/KEY: misc feature  
; LOCATION: (372)..(372)  
; OTHER INFORMATION: Xaa can be any naturally occurring amino acid  
US-11-058-746-10

Query Match 35.2%; Score 32; DB 7; Length 372;  
Best Local Similarity 54.5%; Pred. No. 54;  
Matches 6; Conservative 2; Mismatches 3; Indels 0; Gaps 0;

QY 7 YSRRRFSTGTG 17  
||| :||  
Db 129 YSHRRHSNTG 139

RESULT 13  
US-11-058-746-6  
; Sequence 6, Application US/11058746  
; Publication No. US20060101543A1  
; GENERAL INFORMATION:  
; APPLICANT: Somerville, Chris  
; APPLICANT: Broun, Pierre  
; APPLICANT: Van de Loo, Frank  
; APPLICANT: Boddupalli, Sekhar S  
; TITLE OF INVENTION: PRODUCTION OF HYDROXYLATED PATTY ACIDS IN GENETICALLY MODIFIED  
; FILE REFERENCE: 56100-5022-12  
; CURRENT APPLICATION NUMBER: US/11/058,746  
; PRIOR FILING DATE: 2005-02-16  
; PRIOR APPLICATION NUMBER: US 08/597,313  
; PRIOR FILING DATE: 1996-02-06  
; PRIOR APPLICATION NUMBER: US 08/530,862  
; PRIOR FILING DATE: 1995-09-20  
; PRIOR APPLICATION NUMBER: US 08/320,982  
; PRIOR FILING DATE: 1994-10-11  
; PRIOR APPLICATION NUMBER: US 08/314,596  
; PRIOR FILING DATE: 1994-09-26  
; PRIOR APPLICATION NUMBER: PCT/US95/11855  
; PRIOR FILING DATE: 1995-09-25  
; NUMBER OF SEQ ID NOS: 15  
; SOFTWARE: PatentIn version 3.3  
; SEQ ID NO 6  
; LENGTH: 383  
; TYPE: PRT  
; ORGANISM: Arabidopsis thaliana  
US-11-058-746-6

Query Match 35.2%; Score 32; DB 7; Length 383;  
Best Local Similarity 54.5%; Pred. No. 56;  
Matches 6; Conservative 2; Mismatches 3; Indels 0; Gaps 0;

QY 7 YSRRRFSTGTG 17  
||| :||  
Db 139 YSHRRHSNTG 149

RESULT 14  
US-11-058-746-7  
; Sequence 7, Application US/11058746  
; Publication No. US20060101543A1  
; GENERAL INFORMATION:

; APPLICANT: Somerville, Chris  
; APPLICANT: Broun, Pierre  
; APPLICANT: Van de Loo, Frank  
; APPLICANT: Boddupalli, Sekhar S  
; TITLE OF INVENTION: PRODUCTION OF HYDROXYLATED PATTY ACIDS IN GENETICALLY MODIFIED  
; FILE REFERENCE: 56100-5022-12  
; CURRENT APPLICATION NUMBER: US/11/058,746  
; PRIOR FILING DATE: 2005-02-16  
; PRIOR APPLICATION NUMBER: US 08/597,313  
; PRIOR FILING DATE: 1996-02-06  
; PRIOR APPLICATION NUMBER: US 08/530,862  
; PRIOR FILING DATE: 1995-09-20  
; PRIOR APPLICATION NUMBER: US 08/320,982  
; PRIOR FILING DATE: 1994-10-11  
; PRIOR APPLICATION NUMBER: US 08/314,596  
; PRIOR FILING DATE: 1994-09-26  
; PRIOR APPLICATION NUMBER: PCT/US95/11855  
; PRIOR FILING DATE: 1995-09-25  
; NUMBER OF SEQ ID NOS: 15  
; SOFTWARE: PatentIn version 3.3  
; SEQ ID NO 7  
; LENGTH: 384  
; TYPE: PRT  
; ORGANISM: Brassica napus  
; FEATURE:  
; NAME/KEY: misc feature  
; LOCATION: (384)..(384)  
; OTHER INFORMATION: Xaa can be any naturally occurring amino acid  
US-11-058-746-7

Query Match 35.2%; Score 32; DB 7; Length 384;  
Best Local Similarity 54.5%; Pred. No. 56;  
Matches 6; Conservative 2; Mismatches 3; Indels 0; Gaps 0;

QY 7 YSRRRFSTGTG 17  
||| :||  
Db 139 YSHRRHSNTG 149

RESULT 15  
US-11-249-111-96  
; Sequence 96, Application US/11249111  
; Publication No. US20060099623A1  
; GENERAL INFORMATION:  
; APPLICANT: Glenn, Matthew  
; APPLICANT: Lubbers, Mark W  
; APPLICANT: Dekker, James  
; TITLE OF INVENTION: Polynucleotides and polypeptides isolated from Lactobacillus  
; FILE REFERENCE: 13353.1048u1c2  
; CURRENT APPLICATION NUMBER: US/11/249,111  
; PRIOR FILING DATE: 2005-10-11  
; PRIOR APPLICATION NUMBER: 10/288,930  
; PRIOR FILING DATE: 2002-11-05  
; PRIOR APPLICATION NUMBER: 09/724,623  
; PRIOR FILING DATE: 2000-11-28  
; PRIOR APPLICATION NUMBER: 60/148,801  
; PRIOR FILING DATE: 1999-12-02  
; NUMBER OF SEQ ID NOS: 124  
; SOFTWARE: FastSeq for Windows Version 4.0  
; SEQ ID NO 96  
; LENGTH: 640  
; TYPE: PRT  
; ORGANISM: Lactobacillus rhamnosus  
; FEATURE:  
; NAME/KEY: VARIANT  
; LOCATION: (1)...(640)  
; OTHER INFORMATION: Xaa = Any Amino Acid  
US-11-249-111-96

Query Match 35.2%; Score 32; DB 7; Length 640;  
Best Local Similarity 46.2%; Pred. No. 1e+02;

Matches 6; Conservative 2; Mismatches 5; Indels 0; Gaps 0;

QY 4 RLSYSRRRSTST 16  
:|: ||| |  
Db 201 QLGFKLRFRKTGT 213

RESULT 16  
US-10-505-928-357  
; Sequence 357, Application US/10505928  
; Publication No. US20060088532A1  
; GENERAL INFORMATION:  
; APPLICANT: Ludwig Institute for Cancer Research et al.  
; TITLE OF INVENTION: LYMPHATIC ENDOTHELIAL GENES  
; FILE REFERENCE: 28967/39178  
; CURRENT APPLICATION NUMBER: US/10/505,928  
; PRIOR FILING DATE: 2004-08-27  
; PRIOR APPLICATION NUMBER: US 60/363,019  
; PRIOR FILING DATE: 2002-03-07  
; NUMBER OF SEQ ID NOS: 866  
; SOFTWARE: PatentIn 3.2  
; SEQ ID NO 357  
; LENGTH: 3256  
; TYPE: PRT  
; ORGANISM: Homo sapiens  
US-10-505-928-357

Query Match 35.2%; Score 32; DB 6; Length 3256;  
Best Local Similarity 54.5%; Pred. No. 6.5e+02;  
Matches 6; Conservative 2; Mismatches 3; Indels 0; Gaps 0;

QY 8 SRRRSTSTGR 18  
:|: ||| |  
Db 1629 SKRLKTSLSGK 1639

RESULT 17  
US-10-505-928-648  
; Sequence 648, Application US/10505928  
; Publication No. US20060088532A1  
; GENERAL INFORMATION:  
; APPLICANT: Ludwig Institute for Cancer Research et al.  
; TITLE OF INVENTION: LYMPHATIC ENDOTHELIAL GENES  
; FILE REFERENCE: 28967/39178  
; CURRENT APPLICATION NUMBER: US/10/505,928  
; PRIOR FILING DATE: 2004-08-27  
; PRIOR APPLICATION NUMBER: US 60/363,019  
; PRIOR FILING DATE: 2002-03-07  
; NUMBER OF SEQ ID NOS: 866  
; SOFTWARE: PatentIn 3.2  
; SEQ ID NO 648  
; LENGTH: 180  
; TYPE: PRT  
; ORGANISM: Homo sapiens  
US-10-505-928-648

Query Match 34.1%; Score 31; DB 6; Length 180;  
Best Local Similarity 66.7%; Pred. No. 36;  
Matches 8; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

QY 6 SYSRRRSTSTG 17  
:|: ||| |  
Db 34 SSSRRRRSCCTG 45

RESULT 18  
US-11-266-747-434  
; Sequence 434, Application US/11266747  
; Publication No. US2006009700A1  
; GENERAL INFORMATION:  
; APPLICANT: Davis, S. Christopher  
; APPLICANT: Fox, Richard J.  
; APPLICANT: Gavrilovic, Vesna

; APPLICANT: Huisman, Gjalte W.  
; APPLICANT: Mundorff, Emily C.  
; APPLICANT: Newman, Lisa M.  
; TITLE OF INVENTION: Improved Halohydrin Dehalogenases and Related Polynucleotides  
; FILE REFERENCE: 16028US05 0353.510US  
; CURRENT APPLICATION NUMBER: US/11/266,747  
; CURRENT FILING DATE: 2005-11-02  
; PRIOR APPLICATION NUMBER: 11/067,323  
; PRIOR FILING DATE: 2005-02-23  
; PRIOR APPLICATION NUMBER: 10/917,179  
; PRIOR FILING DATE: 2004-08-11  
; PRIOR APPLICATION NUMBER: 60/546,033  
; PRIOR FILING DATE: 2004-02-18  
; PRIOR APPLICATION NUMBER: 60/494,382  
; PRIOR FILING DATE: 2003-08-11  
; NUMBER OF SEQ ID NOS: 2848  
; SOFTWARE: PatentIn version 3.3  
; SEQ ID NO 434  
; LENGTH: 235  
; TYPE: PRT  
; ORGANISM: Artificial Sequence  
; FEATURE:  
; OTHER INFORMATION: Synthetic Construct  
US-11-266-747-434

Query Match 34.1%; Score 31; DB 7; Length 235;  
Best Local Similarity 54.5%; Pred. No. 49;  
Matches 6; Conservative 2; Mismatches 3; Indels 0; Gaps 0;

QY 3 GRLYSRRRFS 13  
:|: ||| |  
Db 135 GALAYSTARFA 145

RESULT 19  
US-11-264-784-34  
; Sequence 34, Application US/11264784  
; Publication No. US20060094092A1  
; GENERAL INFORMATION:  
; APPLICANT: E.I. duPont de Nemours & Co., Inc.  
; APPLICANT: Damude, Howard Glenn  
; APPLICANT: Gillies, Peter John  
; APPLICANT: Macool, Daniel Joseph  
; APPLICANT: Picataggio, Stephen K.  
; APPLICANT: Pollak, Dana M. Walters  
; APPLICANT: Ragghianti, James John  
; APPLICANT: Xue, Zhixiong  
; APPLICANT: Yadav, Narendra S.  
; APPLICANT: Zhang, Hongxiang  
; APPLICANT: Zhu, Quinn  
; TITLE OF INVENTION: HIGH ARACHIDONIC ACID PRODUCING STRAINS OF YARROWIA LIPOLYTICA  
; FILE REFERENCE: CL3136 USNA  
; CURRENT APPLICATION NUMBER: US/11/264,784  
; CURRENT FILING DATE: 2005-11-01  
; NUMBER OF SEQ ID NOS: 375  
; SOFTWARE: PatentIn version 3.3  
; SEQ ID NO 34  
; LENGTH: 551  
; TYPE: PRT  
; ORGANISM: Magnaporthe grisea  
US-11-264-784-34

Query Match 34.1%; Score 31; DB 7; Length 551;  
Best Local Similarity 50.0%; Pred. No. 1.3e+02;  
Matches 8; Conservative 1; Mismatches 7; Indels 0; Gaps 0;

QY 1 RGGRLYSRRRFRSTST 16  
:|: ||| |  
Db 512 RGGQSLKVRNQRST 527

RESULT 20  
US-10-505-928-416

```
; Sequence 416, Application US/10505928
; Publication No. US20060088532A1
; GENERAL INFORMATION:
; APPLICANT: Ludwig Institute for Cancer Research et al.
; TITLE OF INVENTION: LYMPHATIC ENDOTHELIAL GENES
; FILE REFERENCE: 28967/39178
; CURRENT APPLICATION NUMBER: US/10/505,928
; CURRENT FILING DATE: 2004-08-27
; PRIOR APPLICATION NUMBER: US 60/363,019
; PRIOR FILING DATE: 2002-03-07
; NUMBER OF SEQ ID NOS: 866
; SOFTWARE: PatentIn 3.2
; SEQ ID NO 416
; LENGTH: 708
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-505-928-416

Query Match      34.1%; Score 31; DB 6; Length 708;
Best Local Similarity 44.4%; Pred. No. 1.7e+02;
Matches 8; Conservative 1; Mismatches 9; Indels 0; Gaps 0;

QY      1 RGGRLSYRRRFFSTGCR 18
      ||||| | | | | |
Db      577 RGGGQNSASRGSGQR 594

RESULT 21
US-11-261-384-2
; Sequence 2, Application US/11261384
; Publication No. US20060095979A1
; GENERAL INFORMATION:
; APPLICANT: Allen, Keith D.
; TITLE OF INVENTION: TRANSGENIC MICE CONTAINING CLCN4
; FILE REFERENCE: R-890
; CURRENT APPLICATION NUMBER: US/11/261,384
; CURRENT FILING DATE: 2005-10-27
; PRIOR APPLICATION NUMBER: US/10/109,562
; PRIOR FILING DATE: 2002-03-28
; PRIOR APPLICATION NUMBER: US 60/280,312
; PRIOR FILING DATE: 2001-03-29
; PRIOR APPLICATION NUMBER: US 60/324,640
; PRIOR FILING DATE: 2001-09-24
; NUMBER OF SEQ ID NOS: 4
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 2
; LENGTH: 747
; TYPE: PRT
; ORGANISM: Mus musculus
US-11-261-384-2

Query Match      34.1%; Score 31; DB 7; Length 747;
Best Local Similarity 42.9%; Pred. No. 1.8e+02;
Matches 6; Conservative 4; Mismatches 4; Indels 0; Gaps 0;

QY      5 LSYRRRFFSTGCR 18
      ::::| | | | |
Db      341 IAWCRKRKTRLCR 354

RESULT 22
US-10-511-455-54
; Sequence 52, Application US/10511455
; Publication No. US20060088835A1
; GENERAL INFORMATION:
; APPLICANT: Pickard, Benjamin Simon
; APPLICANT: Blackwood, Douglas
; APPLICANT: Porteous, David
; APPLICANT: Muir, Walter John
; APPLICANT: Mors, Ole
; APPLICANT: Ewald, Henrik Lykke
; TITLE OF INVENTION: SCHIZOPHRENIA ASSOCIATED GENES
; FILE REFERENCE: 9013.63
; CURRENT APPLICATION NUMBER: US/10/511,455
; CURRENT FILING DATE: 2004-10-05
; PRIOR APPLICATION NUMBER: PCT/GB03/001543
; PRIOR FILING DATE: 2003-04-07
; PRIOR APPLICATION NUMBER: GB0207902.8
; PRIOR FILING DATE: 2002-04-05
; PRIOR APPLICATION NUMBER: GB0207904.4
; PRIOR FILING DATE: 2002-04-05
; PRIOR APPLICATION NUMBER: GB0207900.2
; PRIOR FILING DATE: 2002-04-05
; PRIOR APPLICATION NUMBER: GB0207901.0
; PRIOR FILING DATE: 2002-04-05
; PRIOR APPLICATION NUMBER: GB0227734.1
; PRIOR FILING DATE: 2002-11-28
; NUMBER OF SEQ ID NOS: 94
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 54
; LENGTH: 938
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-511-455-54

Query Match      34.1%; Score 31; DB 6; Length 938;
Best Local Similarity 50.0%; Pred. No. 2.4e+02;
Matches 8; Conservative 4; Mismatches 2; Indels 2; Gaps 1;
```

```
; FILE REFERENCE: 9013.63
; CURRENT APPLICATION NUMBER: US/10/511,455
; CURRENT FILING DATE: 2004-10-05
; PRIOR APPLICATION NUMBER: PCT/GB03/001543
; PRIOR FILING DATE: 2003-04-07
; PRIOR APPLICATION NUMBER: GB0207902.8
; PRIOR FILING DATE: 2002-04-05
; PRIOR APPLICATION NUMBER: GB0207904.4
; PRIOR FILING DATE: 2002-04-05
; PRIOR APPLICATION NUMBER: GB0207900.2
; PRIOR FILING DATE: 2002-04-05
; PRIOR APPLICATION NUMBER: GB0207901.0
; PRIOR FILING DATE: 2002-04-05
; PRIOR APPLICATION NUMBER: GB0227734.1
; PRIOR FILING DATE: 2002-11-28
; NUMBER OF SEQ ID NOS: 94
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 52
; LENGTH: 901
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-511-455-52

Query Match      34.1%; Score 31; DB 6; Length 901;
Best Local Similarity 50.0%; Pred. No. 2.3e+02;
Matches 8; Conservative 4; Mismatches 2; Indels 2; Gaps 1;

QY      1 RGGRLSYRRRFFSTST 16
      :||| | | | | | | | |
Db      576 KGG--SASRRRLSSAS 589

RESULT 23
US-10-511-455-54
; Sequence 54, Application US/10511455
; Publication No. US20060088835A1
; GENERAL INFORMATION:
; APPLICANT: Pickard, Benjamin Simon
; APPLICANT: Blackwood, Douglas
; APPLICANT: Porteous, David
; APPLICANT: Muir, Walter John
; APPLICANT: Mors, Ole
; APPLICANT: Ewald, Henrik Lykke
; TITLE OF INVENTION: SCHIZOPHRENIA ASSOCIATED GENES
; FILE REFERENCE: 9013.63
; CURRENT APPLICATION NUMBER: US/10/511,455
; CURRENT FILING DATE: 2004-10-05
; PRIOR APPLICATION NUMBER: PCT/GB03/001543
; PRIOR FILING DATE: 2003-04-07
; PRIOR APPLICATION NUMBER: GB0207902.8
; PRIOR FILING DATE: 2002-04-05
; PRIOR APPLICATION NUMBER: GB0207904.4
; PRIOR FILING DATE: 2002-04-05
; PRIOR APPLICATION NUMBER: GB0207900.2
; PRIOR FILING DATE: 2002-04-05
; PRIOR APPLICATION NUMBER: GB0207901.0
; PRIOR FILING DATE: 2002-04-05
; PRIOR APPLICATION NUMBER: GB0227734.1
; PRIOR FILING DATE: 2002-11-28
; NUMBER OF SEQ ID NOS: 94
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 54
; LENGTH: 938
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-511-455-54

Query Match      34.1%; Score 31; DB 6; Length 938;
Best Local Similarity 50.0%; Pred. No. 2.4e+02;
Matches 8; Conservative 4; Mismatches 2; Indels 2; Gaps 1;
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```
Db      613 KGG--SASRRRLSSAS 626

RESULT 24
US-10-511-937-2603
; Sequence 2603, Application US/10511937
; Publication No. US20060088836A1
; GENERAL INFORMATION:
; APPLICANT: EXPRESSION DIAGNOSTICS, INC.
; APPLICANT: Wohlgemuth, Jay
; APPLICANT: Fry, Kirk
; APPLICANT: Woodward, Robert
; APPLICANT: Ly, Ngoc
; APPLICANT: Prentice, James
; APPLICANT: Morris, Macdonald
; APPLICANT: Rosenberg, Steven
; TITLE OF INVENTION: METHODS AND COMPOSITIONS FOR DIAGNOSING
; TITLE OF INVENTION: AND MONITORING TRANSPLANT REJECTION
; FILE REFERENCE: 506612000104
; CURRENT APPLICATION NUMBER: US/10/511,937
; CURRENT FILING DATE: 2004-10-19
; PRIOR APPLICATION NUMBER: PCT/US2003/012946
; PRIOR FILING DATE: 2003-04-24
; PRIOR APPLICATION NUMBER: US 10/131,831
; PRIOR FILING DATE: 2002-04-24
; PRIOR APPLICATION NUMBER: US 10/325,899
; PRIOR FILING DATE: 2002-12-20
; NUMBER OF SEQ ID NOS: 3117
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 2603
; LENGTH: 950
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-511-937-2603

Query Match      34.1%; Score 31; DB 6; Length 950;
Best Local Similarity 66.7%; Pred. No. 2.4e+02;
Matches 6; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY      1 RGGRLSYSR 9
      |||||
Db      925 RGGGQGYPR 933

RESULT 25
US-10-512-386-56
; Sequence 56, Application US/10512386
; Publication No. US20060088837A1
; GENERAL INFORMATION:
; APPLICANT: NATIONAL INSTITUTE OF ADVANCED INDUSTRIAL SCIENCE AND TECHNOLOGY
; TITLE OF INVENTION: EXPRESSION SYSTEM FOR STEM-LOOP RNA MOLECULES HAVING RNAI EFFECT
; FILE REFERENCE: GFU-A0203Y1P
; CURRENT APPLICATION NUMBER: US/10/512,386
; CURRENT FILING DATE: 2004-10-25
; PRIOR APPLICATION NUMBER: JP 2002-127089
; PRIOR FILING DATE: 2002-04-26
; PRIOR APPLICATION NUMBER: JP 2003-4706
; PRIOR FILING DATE: 2003-01-10
; PRIOR APPLICATION NUMBER: US 60/449,860
; PRIOR FILING DATE: 2003-02-27
; NUMBER OF SEQ ID NOS: 56
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 56
; LENGTH: 1924
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-512-386-56

Query Match      34.1%; Score 31; DB 6; Length 1924;
Best Local Similarity 66.7%; Pred. No. 5.4e+02;
Matches 6; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

QY      3 GRLSYSRRR 11

Db      613 KGG--SASRRRLSSAS 626

RESULT 26
US-10-501-834-7
; Sequence 7, Application US/10501834
; Publication No. US20060088828A1
; GENERAL INFORMATION:
; APPLICANT: HARRIS, Peter C., Ward, Christopher J., Rossetti, Sandro, and Torres,
; APPLICANT: Vicente E.
; TITLE OF INVENTION: Polycystic Kidney Disease Nucleic Acids
; TITLE OF INVENTION: and Proteins
; FILE REFERENCE: 07039/386US1
; CURRENT APPLICATION NUMBER: US/10/501,834
; CURRENT FILING DATE: 2004-07-19
; PRIOR APPLICATION NUMBER: PCT/US03/02038
; PRIOR FILING DATE: 2003-01-23
; PRIOR APPLICATION NUMBER: 60/351,110
; PRIOR FILING DATE: 2002-01-23
; NUMBER OF SEQ ID NOS: 221
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 7
; LENGTH: 4051
; TYPE: PRT
; ORGANISM: Rattus norvegicus
US-10-501-834-7

Query Match      34.1%; Score 31; DB 6; Length 4051;
Best Local Similarity 70.0%; Pred. No. 1.3e+03;
Matches 7; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY      6 SYSRRRPFSTS 15
      |||||
Db      2256 SYMDRSFSTS 2265

RESULT 27
US-10-501-814-3
; Sequence 3, Application US/10501814
; Publication No. US20060088827A1
; GENERAL INFORMATION:
; APPLICANT: Evotec NeuroSciences GmbH
; TITLE OF INVENTION: Diagnostic and therapeutic use of a voltage-gated ion
; TITLE OF INVENTION: channel for neurodegenerative diseases
; FILE REFERENCE: P67564US1
; CURRENT APPLICATION NUMBER: US/10/501,814
; CURRENT FILING DATE: 2004-07-19
; NUMBER OF SEQ ID NOS: 15
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 3
; LENGTH: 2005
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-501-814-3

Query Match      33.5%; Score 30.5; DB 6; Length 2005;
Best Local Similarity 53.8%; Pred. No. 7e+02;
Matches 7; Conservative 3; Mismatches 2; Indels 1; Gaps 1;

QY      2 GGRLSYSRRRFST 14
      |||||
Db      543 GRLTY-EKRFS 554

RESULT 28
US-11-263-326-131
; Sequence 131, Application US/11263326
; Publication No. US20060089306A1
; GENERAL INFORMATION:
; APPLICANT: Wallace, Robyn H
; APPLICANT: Mulvey, John C
; APPLICANT: Berkovic, Samuel F
```

```
; TITLE OF INVENTION: NEW EPILEPSY MUTATIONS
; FILE REFERENCE: 1386/13/3
; CURRENT APPLICATION NUMBER: US/11/263,326
; CURRENT FILING DATE: 2005-10-31
; PRIOR APPLICATION NUMBER: US 10/482,834
; PRIOR FILING DATE: 2004-10-12
; PRIOR APPLICATION NUMBER: PCT/AU2004/001051
; PRIOR FILING DATE: 2004-08-06
; PRIOR APPLICATION NUMBER: US 10/451,126
; PRIOR FILING DATE: 2003-10-08
; PRIOR APPLICATION NUMBER: PCT/AU2004/001051
; PRIOR FILING DATE: 2004-08-06
; PRIOR APPLICATION NUMBER: US 10/451,126
; PRIOR FILING DATE: 2003-10-08
; NUMBER OF SEQ ID NOS: 179
; SOFTWARE: PatentIn version 3.3
; SEQ ID NO 131
; LENGTH: 2005
; TYPE: PRT
; ORGANISM: Homo sapiens
US-11-263-326-131

Query Match      33.5%; Score 30.5; DB 7; Length 2005;
Best Local Similarity 53.8%; Pred. No. 7e+02; 2; Indels 1; Gaps 1;
Matches 7; Conservative 3; Mismatches 2;

Qy      2 GGRLSYRRRPFST 14
Db      543 GSRLTY-EKRFSS 554

RESULT 29
US-11-263-326-132
; Sequence 132, Application US/11263326
; Publication No. US20060089306A1
; GENERAL INFORMATION:
; APPLICANT: Wallace, Robyn H
; APPLICANT: Mulley, John C
; APPLICANT: Berkovic, Samuel F
; TITLE OF INVENTION: NEW EPILEPSY MUTATIONS
; FILE REFERENCE: 1386/13/3
; CURRENT APPLICATION NUMBER: US/11/263,326
; CURRENT FILING DATE: 2005-10-31
; PRIOR APPLICATION NUMBER: US 10/482,834
; PRIOR FILING DATE: 2004-10-12
; PRIOR APPLICATION NUMBER: PCT/AU2004/001051
; PRIOR FILING DATE: 2004-08-06
; PRIOR APPLICATION NUMBER: US 10/451,126
; PRIOR FILING DATE: 2003-10-08
; NUMBER OF SEQ ID NOS: 179
; SOFTWARE: PatentIn version 3.3
; SEQ ID NO 132
; LENGTH: 2005
; TYPE: PRT
; ORGANISM: Homo sapiens
US-11-263-326-132

Query Match      33.5%; Score 30.5; DB 7; Length 2005;
Best Local Similarity 53.8%; Pred. No. 7e+02; 2; Indels 1; Gaps 1;
Matches 7; Conservative 3; Mismatches 2;

Qy      2 GGRLSYRRRPFST 14
Db      543 GSRLTY-EKRFSS 554

RESULT 30
US-11-263-326-133
; Sequence 133, Application US/11263326
; Publication No. US20060089306A1
; GENERAL INFORMATION:
; APPLICANT: Wallace, Robyn H
; APPLICANT: Mulley, John C
; APPLICANT: Berkovic, Samuel F
; TITLE OF INVENTION: NEW EPILEPSY MUTATIONS
; FILE REFERENCE: 1386/13/3
; CURRENT APPLICATION NUMBER: US/11/263,326
; CURRENT FILING DATE: 2005-10-31
; PRIOR APPLICATION NUMBER: US 10/482,834
; PRIOR FILING DATE: 2004-10-12
; PRIOR APPLICATION NUMBER: PCT/AU2004/001051
; PRIOR FILING DATE: 2004-08-06
; PRIOR APPLICATION NUMBER: US 10/451,126
; PRIOR FILING DATE: 2003-10-08
; NUMBER OF SEQ ID NOS: 179
; SOFTWARE: PatentIn version 3.3
; SEQ ID NO 133
; LENGTH: 2005
; TYPE: PRT
; ORGANISM: Homo sapiens
US-11-263-326-133

Query Match      33.5%; Score 30.5; DB 7; Length 2005;
Best Local Similarity 53.8%; Pred. No. 7e+02; 2; Indels 1; Gaps 1;
Matches 7; Conservative 3; Mismatches 2;

Qy      2 GGRLSYRRRPFST 14
Db      543 GSRLTY-EKRFSS 554

RESULT 31
US-11-263-326-175
; Sequence 175, Application US/11263326
; Publication No. US20060089306A1
; GENERAL INFORMATION:
; APPLICANT: Wallace, Robyn H
; APPLICANT: Mulley, John C
; APPLICANT: Berkovic, Samuel F
; TITLE OF INVENTION: NEW EPILEPSY MUTATIONS
; FILE REFERENCE: 1386/13/3
; CURRENT APPLICATION NUMBER: US/11/263,326
; CURRENT FILING DATE: 2005-10-31
; PRIOR APPLICATION NUMBER: US 10/482,834
; PRIOR FILING DATE: 2004-10-12
; PRIOR APPLICATION NUMBER: PCT/AU2004/001051
; PRIOR FILING DATE: 2004-08-06
; PRIOR APPLICATION NUMBER: US 10/451,126
; PRIOR FILING DATE: 2003-10-08
; NUMBER OF SEQ ID NOS: 179
; SOFTWARE: PatentIn version 3.3
; SEQ ID NO 175
; LENGTH: 2005
; TYPE: PRT
; ORGANISM: Homo sapiens
US-11-263-326-175

Query Match      33.5%; Score 30.5; DB 7; Length 2005;
Best Local Similarity 53.8%; Pred. No. 7e+02; 2; Indels 1; Gaps 1;
Matches 7; Conservative 3; Mismatches 2;

Qy      2 GGRLSYRRRPFST 14
Db      543 GSRLTY-EKRFSS 554

RESULT 32
US-11-263-326-176
; Sequence 176, Application US/11263326
; Publication No. US20060089306A1
; GENERAL INFORMATION:
; APPLICANT: Wallace, Robyn H
; APPLICANT: Mulley, John C
; APPLICANT: Berkovic, Samuel F
; TITLE OF INVENTION: NEW EPILEPSY MUTATIONS
; FILE REFERENCE: 1386/13/3
; CURRENT APPLICATION NUMBER: US/11/263,326
; CURRENT FILING DATE: 2005-10-31
; PRIOR APPLICATION NUMBER: US 10/482,834
; PRIOR FILING DATE: 2004-10-12
```

; PRIOR APPLICATION NUMBER: PCT/AU2004/001051  
; PRIOR FILING DATE: 2004-08-06  
; PRIOR APPLICATION NUMBER: US 10/451,126  
; PRIOR FILING DATE: 2003-10-08  
; NUMBER OF SEQ ID NOS: 179  
; SOFTWARE: PatentIn version 3.3  
; SEQ ID NO 176  
; LENGTH: 2005  
; TYPE: PRT  
; ORGANISM: Homo sapiens  
US-11-263-326-176

Query Match 33.5%; Score 30.5; DB 7; Length 2005;  
Best Local Similarity 53.8%; Pred. No. 7e+02; 2; Indels 1; Gaps 1;  
Matches 7; Conservative 3; Mismatches 2; Indels 1; Gaps 1;

QY 2 GGRLSYRRRFFST 14  
Db 543 GSRLLTY-EKRFSS 554

RESULT 33  
US-11-263-326-177  
; Sequence 177, Application US/11263326  
; Publication No. US20060089306A1  
; GENERAL INFORMATION:  
; APPLICANT: Wallace, Robyn H  
; APPLICANT: Mulley, John C  
; APPLICANT: Berkovic, Samuel F  
; TITLE OF INVENTION: NEW EPILEPSY MUTATIONS  
; FILE REFERENCE: 1386/13/3  
; CURRENT APPLICATION NUMBER: US/11/263,326  
; CURRENT FILING DATE: 2005-10-31  
; PRIOR APPLICATION NUMBER: US 10/482,834  
; PRIOR FILING DATE: 2004-10-12  
; PRIOR APPLICATION NUMBER: PCT/AU2004/001051  
; PRIOR FILING DATE: 2004-08-06  
; PRIOR APPLICATION NUMBER: US 10/451,126  
; PRIOR FILING DATE: 2003-10-08  
; NUMBER OF SEQ ID NOS: 179  
; SOFTWARE: PatentIn version 3.3  
; SEQ ID NO 177  
; LENGTH: 2005  
; TYPE: PRT  
; ORGANISM: Homo sapiens  
US-11-263-326-177

Query Match 33.5%; Score 30.5; DB 7; Length 2005;  
Best Local Similarity 53.8%; Pred. No. 7e+02; 2; Indels 1; Gaps 1;  
Matches 7; Conservative 3; Mismatches 2; Indels 1; Gaps 1;

QY 2 GGRLSYRRRFFST 14  
Db 543 GSRLLTY-EKRFSS 554

RESULT 34  
US-11-263-326-178  
; Sequence 178, Application US/11263326  
; Publication No. US20060089306A1  
; GENERAL INFORMATION:  
; APPLICANT: Wallace, Robyn H  
; APPLICANT: Mulley, John C  
; APPLICANT: Berkovic, Samuel F  
; TITLE OF INVENTION: NEW EPILEPSY MUTATIONS  
; FILE REFERENCE: 1386/13/3  
; CURRENT APPLICATION NUMBER: US/11/263,326  
; CURRENT FILING DATE: 2005-10-31  
; PRIOR APPLICATION NUMBER: US 10/482,834  
; PRIOR FILING DATE: 2004-10-12  
; PRIOR APPLICATION NUMBER: PCT/AU2004/001051  
; PRIOR FILING DATE: 2004-08-06  
; PRIOR APPLICATION NUMBER: US 10/451,126

; PRIOR FILING DATE: 2003-10-08  
; NUMBER OF SEQ ID NOS: 179  
; SOFTWARE: PatentIn version 3.3  
; SEQ ID NO 178  
; LENGTH: 2005  
; TYPE: PRT  
; ORGANISM: Homo sapiens  
US-11-263-326-178

Query Match 33.5%; Score 30.5; DB 7; Length 2005;  
Best Local Similarity 53.8%; Pred. No. 7e+02; 2; Indels 1; Gaps 1;  
Matches 7; Conservative 3; Mismatches 2; Indels 1; Gaps 1;

QY 2 GGRLSYRRRFFST 14  
Db 543 GSRLLTY-EKRFSS 554

RESULT 35  
US-11-263-326-179  
; Sequence 179, Application US/11263326  
; Publication No. US20060089306A1  
; GENERAL INFORMATION:  
; APPLICANT: Wallace, Robyn H  
; APPLICANT: Mulley, John C  
; APPLICANT: Berkovic, Samuel F  
; TITLE OF INVENTION: NEW EPILEPSY MUTATIONS  
; FILE REFERENCE: 1386/13/3  
; CURRENT APPLICATION NUMBER: US/11/263,326  
; CURRENT FILING DATE: 2005-10-31  
; PRIOR APPLICATION NUMBER: US 10/482,834  
; PRIOR FILING DATE: 2004-10-12  
; PRIOR APPLICATION NUMBER: PCT/AU2004/001051  
; PRIOR FILING DATE: 2004-08-06  
; PRIOR APPLICATION NUMBER: US 10/451,126  
; PRIOR FILING DATE: 2003-10-08  
; NUMBER OF SEQ ID NOS: 179  
; SOFTWARE: PatentIn version 3.3  
; SEQ ID NO 179  
; LENGTH: 2005  
; TYPE: PRT  
; ORGANISM: Homo sapiens  
US-11-263-326-179

Query Match 33.5%; Score 30.5; DB 7; Length 2005;  
Best Local Similarity 53.8%; Pred. No. 7e+02; 2; Indels 1; Gaps 1;  
Matches 7; Conservative 3; Mismatches 2; Indels 1; Gaps 1;

QY 2 GGRLSYRRRFFST 14  
Db 543 GSRLLTY-EKRFSS 554

RESULT 36  
US-11-301-924-24  
; Sequence 24, Application US/11301924  
; Publication No. US20060090218A1  
; GENERAL INFORMATION:  
; APPLICANT: Joshua Z. Levin  
; APPLICANT: Ken Phillips  
; APPLICANT: Greg Budziszewski  
; APPLICANT: Fred Meins  
; APPLICANT: Zhenya Glazov  
; TITLE OF INVENTION: Methods of Controlling Gene Expression  
; FILE REFERENCE: 3148USNP  
; CURRENT APPLICATION NUMBER: US/11/301,924  
; CURRENT FILING DATE: 2005-12-13  
; PRIOR APPLICATION NUMBER: US/09/896,186  
; PRIOR FILING DATE: 2001-06-29  
; PRIOR APPLICATION NUMBER: 60/222,202  
; PRIOR FILING DATE: 2000-08-01  
; NUMBER OF SEQ ID NOS: 34  
; SOFTWARE: PatentIn Ver. 2.1



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; SEQ ID NO 24
; LENGTH: 288
; TYPE: PRT
; ORGANISM: Arabidopsis thaliana
US-11-301-924-24

Query Match      33.0%; Score 30; DB 7; Length 288;
Best Local Similarity 62.5%; Pred. No. 94;
Matches 5; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

Qy      2 GGRLSYSR 9
Db      95 GGRILYSK 102

RESULT 37
US-11-246-957-16
; Sequence 16, Application US/11246957
; Publication No. US20060093621A1
; GENERAL INFORMATION:
; APPLICANT: Bandara, Aloka
; APPLICANT: Boyle, Stephen
; APPLICANT: Sriranganathan, Nammalwar
; APPLICANT: Schurig, Gerhardt
; TITLE OF INVENTION: Development of a Live, Attenuated, Recombinant Vaccine for
; TITLE OF INVENTION: Brucellosis
; FILE REFERENCE: 01640446pa
; CURRENT FILING DATE: 2005-10-11
; PRIOR APPLICATION NUMBER: US/11/246,957
; PRIOR FILING DATE: 2004-02-06
; PRIOR APPLICATION NUMBER: US60/541,954
; PRIOR FILING DATE: 2005-02-04
; PRIOR FILING DATE: 2005-02-04
; NUMBER OF SEQ ID NOS: 20
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 16
; LENGTH: 298
; TYPE: PRT
; ORGANISM: Bradyrhizobium japonicum
US-11-246-957-16

Query Match      33.0%; Score 30; DB 7; Length 298;
Best Local Similarity 37.5%; Pred. No. 98;
Matches 6; Conservative 4; Mismatches 6; Indels 0; Gaps 0;

Qy      3 GRLSYRRRPFSTGTGR 18
Db      282 GALALTARYTTFSGR 297

RESULT 38
US-11-301-924-2
; Sequence 2, Application US/11301924
; Publication No. US20060090218A1
; GENERAL INFORMATION:
; APPLICANT: Joshua Z. Levin
; APPLICANT: Ken Phillips
; APPLICANT: Greg Budziszewski
; APPLICANT: Fred Meins
; APPLICANT: Zhenya Glazov
; TITLE OF INVENTION: Methods of Controlling Gene Expression
; FILE REFERENCE: 31481USNP
; CURRENT APPLICATION NUMBER: US/11/301,924
; CURRENT FILING DATE: 2005-12-13
; PRIOR APPLICATION NUMBER: US/09/896,186
; PRIOR FILING DATE: 2001-06-29
; PRIOR APPLICATION NUMBER: 60/222,202
; PRIOR FILING DATE: 2000-08-01
; NUMBER OF SEQ ID NOS: 34
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 2
; LENGTH: 313
; TYPE: PRT
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; ORGANISM: Arabidopsis thaliana
US-11-301-924-2

Query Match      33.0%; Score 30; DB 7; Length 313;
Best Local Similarity 62.5%; Pred. No. 1e+02;
Matches 5; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

Qy      2 GGRLSYSR 9
Db      95 GGRILYSK 102

RESULT 39
US-10-511-937-2466
; Sequence 2466, Application US/10511937
; Publication No. US20060088836A1
; GENERAL INFORMATION:
; APPLICANT: EXPRESSION DIAGNOSTICS, INC.
; APPLICANT: Wohlgenuth, Jay
; APPLICANT: Fry, Kirk
; APPLICANT: Woodward, Robert
; APPLICANT: Ly, Ngoc
; APPLICANT: Prentice, James
; APPLICANT: Morris, Macdonald
; APPLICANT: Rosenberg, Steven
; TITLE OF INVENTION: METHODS AND COMPOSITIONS FOR DIAGNOSING
; TITLE OF INVENTION: AND MONITORING TRANSPLANT REJECTION
; FILE REFERENCE: 506612000104
; CURRENT APPLICATION NUMBER: US/10/511,937
; CURRENT FILING DATE: 2004-10-19
; PRIOR APPLICATION NUMBER: PCT/US2003/012946
; PRIOR FILING DATE: 2003-04-24
; PRIOR APPLICATION NUMBER: US 10/131,831
; PRIOR FILING DATE: 2002-04-24
; PRIOR APPLICATION NUMBER: US 10/325,899
; PRIOR FILING DATE: 2002-12-20
; NUMBER OF SEQ ID NOS: 3117
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 2466
; LENGTH: 362
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-511-937-2466

Query Match      33.0%; Score 30; DB 6; Length 362;
Best Local Similarity 42.9%; Pred. No. 1.2e+02;
Matches 6; Conservative 4; Mismatches 4; Indels 0; Gaps 0;

Qy      3 GRLSYRRRPFSTST 16
Db      267 GRSWARKQAHT 280

RESULT 40
US-10-511-937-2608
; Sequence 2608, Application US/10511937
; Publication No. US20060088836A1
; GENERAL INFORMATION:
; APPLICANT: EXPRESSION DIAGNOSTICS, INC.
; APPLICANT: Wohlgenuth, Jay
; APPLICANT: Fry, Kirk
; APPLICANT: Woodward, Robert
; APPLICANT: Ly, Ngoc
; APPLICANT: Prentice, James
; APPLICANT: Morris, Macdonald
; APPLICANT: Rosenberg, Steven
; TITLE OF INVENTION: METHODS AND COMPOSITIONS FOR DIAGNOSING
; TITLE OF INVENTION: AND MONITORING TRANSPLANT REJECTION
; FILE REFERENCE: 506612000104
; CURRENT APPLICATION NUMBER: US/10/511,937
; CURRENT FILING DATE: 2004-10-19
; PRIOR APPLICATION NUMBER: PCT/US2003/012946
; PRIOR FILING DATE: 2003-04-24
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; PRIOR APPLICATION NUMBER: US 10/131,831
; PRIOR FILING DATE: 2002-04-24
; PRIOR APPLICATION NUMBER: US 10/325,899
; PRIOR FILING DATE: 2002-12-20
; NUMBER OF SEQ ID NOS: 3117
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 2608
; LENGTH: 362
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-511-937-2608
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Query Match      33.0%; Score 30; DB 6; Length 362;
Best Local Similarity 53.8%; Pred.No. 1.2e+02;
Matches 7; Conservative 1; Mismatches 5; Indels 0; Gaps 0;
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QY      6 SYSRRRFTSTGR 18
      |:|:|:|:|
Db      26 SHSMRYFTTSVR 38
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Search completed: May 21, 2006, 00:39:35
Job time : 10 secs
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GenCore version 5.1.8  
Copyright (c) 1993 - 2006 Bioceleration Ltd.

OM protein - protein search, using sw model

Run on: May 21, 2006, 00:19:21 ; Search time 38 Seconds  
(without alignments)  
45.576 Million cell updates/sec

Title: US-09-857-000a-11

Perfect score: 91

Sequence: 1 RGGRLSYRRRSTSTGR 18

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 283416 seqs, 96216763 residues

Total number of hits satisfying chosen parameters: 283416

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 100 summaries

Database :

1: PIR 80.\*

2: piri.\*

3: pir2.\*

4: pir3.\*

5: pir4.\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

# SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	61	67.0	149	2 S57607	protegrin 1 precu
2	55	60.4	147	2 JN0900	protegrin 2 precu
3	54	59.3	149	2 A53895	protegrin 3 precu
4	54	59.3	149	2 S57609	protegrin 5 precu
5	47	51.6	94	1 B48549	nucleic acid-bind
6	47	51.6	447	2 S53982	hypothetical prote
7	46	50.5	231	2 T32047	hypothetical prote
8	45	49.5	191	1 QOAG6T	hypothetical prote
9	44	48.4	186	2 A30832	hypothetical prote
10	44	48.4	186	2 AC3229	protein 6a [import
11	44	48.4	293	2 D81896	Neisseria meningit
12	44	48.4	413	2 T03240	FLU/LFY protein ho
13	44	48.4	475	2 B89978	glutamy1-trNAGln a
14	44	48.4	532	2 H2730	probable acyl-CoA
15	43	47.3	107	2 J01251	hypothetical 12.6K
16	43	47.3	108	1 WNVTF5	nucleic acid-bind
17	43	47.3	108	2 S12976	12K protein - pota
18	43	47.3	337	2 A10079	probable glycoprot
19	42	46.2	118	2 C72642	hypothetical prote
20	42	46.2	210	2 AB3420	hypothetical phage
21	42	46.2	386	2 A41950	retrovirus-related
22	42	46.2	747	2 T42599	minor capsid prote
23	42	46.2	1016	2 T30942	aminopeptidase (EC
24	42	46.2	1016	2 T30942	aminopeptidase (EC
25	41	45.1	201	2 B72739	hypothetical prote
26	41	45.1	310	2 T43147	hypothetical prote
27	41	45.1	325	2 T38308	hypothetical prote
28	41	45.1	390	2 AC2761	penicillin binding
29	41	45.1	413	2 A97542	D-ala-D-ala-carbox

30	41	45.1	547	2 S53920	SNG1 protein - yea
31	41	45.1	618	2 AC0884	glutathionylpermi
32	41	45.1	619	2 A91113	glutathionylpermi
33	41	45.1	619	2 A85958	glutathionylpermi
34	41	45.1	619	2 A57538	glutathionylpermi
35	40.5	44.5	464	2 A56800	intermediate filam
36	40	44.0	76	2 A87655	ribosomal protein
37	40	44.0	217	2 T33652	hypothetical prote
38	40	44.0	352	2 D96597	hypothetical prote
39	40	44.0	499	2 C85022	hypothetical prote
40	40	44.0	508	1 O4CHC7	steroid 17alpha-mo
41	40	44.0	513	2 T02002	hypothetical prote
42	40	44.0	622	2 A70414	hypothetical prote
43	40	44.0	622	2 I37984	NADH2 dehydrogenas
44	40	44.0	743	2 E71432	keratin 9, type I,
45	40	44.0	901	2 A13592	hypothetical prote
46	40	44.0	1030	2 A16114	DNA topoisomerase
47	40	44.0	1224	2 T26377	hypothetical prote
48	40	44.0	1636	2 T00057	hypothetical prote
49	39.5	43.4	333	2 AC2386	chaperone DnaJ pro
50	39	42.9	51	2 G70154	ribosomal protein
51	39	42.9	105	2 S42214	hydroxymethylgluta
52	39	42.9	105	2 S42213	hydroxymethylgluta
53	39	42.9	119	2 D82387	conserved hypotet
54	39	42.9	159	2 T05656	hypothetical prote
55	39	42.9	188	2 A48024	glycosylphosphatid
56	39	42.9	211	2 C84888	hypothetical prote
57	39	42.9	231	2 AF1838	hypothetical prote
58	39	42.9	245	2 D84179	hypothetical prote
59	39	42.9	262	2 A13518	nitrate reductase
60	39	42.9	351	2 B34768	ORF5 protein - Orf
61	39	42.9	361	2 B82533	translation releas
62	39	42.9	377	2 E83220	hypothetical prote
63	39	42.9	475	2 AD2698	molecular chaperon
64	39	42.9	533	2 D97480	probable heat-shoc
65	39	42.9	661	2 H84406	aconitase [import
66	39	42.9	694	2 F82511	vgrG protein VCA00
67	39	42.9	753	1 WZBEE8	gene 56 protein -
68	39	42.9	865	2 B69074	probable formate d
69	39	42.9	873	2 B87049	conserved hypotet
70	39	42.9	883	2 C83385	hypothetical prote
71	39	42.9	1163	2 D82202	vgrG protein VCI41
72	39	42.9	2248	2 A35938	profilaggrin - hum
73	38	41.8	135	2 C95422	TRM2011-2a transpo
74	38	41.8	135	2 B95386	TRM2011-2a transpo
75	38	41.8	135	2 A95263	TRM2011-2a transpo
76	38	41.8	135	2 H95878	probable ISM2011-
77	38	41.8	135	2 C96026	probable transposa
78	38	41.8	136	2 E95401	TRM2011-2a transpo
79	38	41.8	149	2 B53895	protegrin 4 precu
80	38	41.8	182	2 A02947	keratin, 60K type
81	38	41.8	213	2 T01464	hypothetical prote
82	38	41.8	218	2 E85021	hypothetical prote
83	38	41.8	276	2 D70817	hypothetical prote
84	38	41.8	313	2 A84444	filaggrin precurs
85	38	41.8	341	2 H83572	O-sialoglycoprotei
86	38	41.8	438	2 A57219	Batten disease-rel
87	38	41.8	438	2 C69431	signal-transducin
88	38	41.8	476	2 AB1294	glutamy1-tRNA (Gln)
89	38	41.8	476	2 AH1665	glutamy1-tRNA (Gln)
90	38	41.8	488	2 E86645	Glu-tRNA amidotran
91	38	41.8	491	2 T21421	hypothetical prote
92	38	41.8	529	1 H70736	IMP dehydrogenase
93	38	41.8	558	2 T50595	probable alkaline
94	38	41.8	590	2 A29904	keratin 5, type II
95	38	41.8	902	2 D84970	ribonuclease 8 [im
96	37.5	41.2	196	2 E84638	probable RS2p22 sp
97	37.5	41.2	358	2 I38121	protein kinase - h
98	37	40.7	219	1 TRPGA2	azurocidin - pig
99	37	40.7	219	2 C69439	sugar fermentation
100	37	40.7	315	2 D84139	mannose-6-phosphat

## ALIGNMENTS

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RESULT 1
S57607
  protegrin 1 precursor - pig
N/Alternate names: neutrophil peptide 1
C/Species: Sus scrofa domestica (domestic pig)
C/Date: 19-Oct-1995 #sequence_revision 03-Nov-1995 #text_change 09-Jul-2004
C/Accession: S66284; S45712; S36820; S34585; S57607
R/Zhao, C.; Ganz, T.; Lehrer, R.I.
FEBS Lett. 368, 197-202, 1995
A/Title: The structure of porcine protegrin genes.
A/Reference number: S66284; MUID:95354835; PMID:7628604
A/Accession: S66284
A/Molecule type: DNA
A/Residues: 1-149 <ZHA>
A/Cross-references: UNIPROT:P32194; UNIPARC:UPI0000131775; EMBL:X84094; NID:g887642; PID:
R/Zhao, C.; Liu, L.; Lehrer, R.I.
FEBS Lett. 346, 285-288, 1994
A/Title: Identification of a new member of the protegrin family by cDNA cloning.
A/Reference number: S45712; MUID:94283613; PMID:8013647
A/Accession: S45712
A/Molecule type: mRNA
A/Residues: 1-149 <ZH2>
A/Cross-references: UNIPARC:UPI0000131775; GB:X79868; NID:g603035; PIDN:CAAS6251.1; PID:
R/Mirgorodskaya, O.A.; Shevchenko, A.A.; Abdalla, K.O.M.A.; Chernushevich, I.V.; Egorov,
FEBS Lett. 330, 339-342, 1993
A/Title: Primary structure of three cationic peptides from porcine neutrophils. Sequence
A/Reference number: S36820; MUID:93387466; PMID:8375505
A/Accession: S36820
A/Molecule type: protein
A/Residues: 131-148 <MIR>
A/Cross-references: UNIPARC:UPI000014310F
R/Kokryakov, V.N.; Harwig, S.S.L.; Panyutich, E.A.; Shevchenko, A.A.; Alekhina, G.M.; Sha
FEBS Lett. 327, 231-236, 1993
A/Title: Protegrins: leukocyte antimicrobial peptides that combine features of corticost
A/Reference number: S34585; MUID:93327946; PMID:8335113
A/Accession: S34586
A/Molecule type: protein
A/Residues: 131-146 <KOK>
A/Cross-references: UNIPARC:UPI000014310F
C/Comment: This protein plays a role in the nonoxidative antimicrobial defense mechanism
C/Superfamily: cathelin; cystatin homology
C/Keywords: amidated carboxyl end; antibacterial; neutrophil
F/1-29/Domain: signal sequence #status predicted <SIG>
F/22-129/Domain: cystatin homology <CYS>
F/131-146/Product: protegrin 2 #status experimental <MAT>
F/146/Modified site: amidated carboxyl end (Val) (amide in mature form from following gl
Query Match 67.0%; Score 61; DB 2; Length 149;
Best Local Similarity 66.7%; Pred. No. 0.0087;
Matches 12; Conservative 0; Mismatches 6; Indels 0; Gaps 0;

QY 1 RGGRLSYRRRFTSTGR 18
Db 131 RGGRLCYRRRFCVGR 148

RESULT 2
JN0900
  protegrin 2 precursor - pig
N/Alternate names: cathelin-like protein precursor; neutrophil peptide 3
C/Species: Sus scrofa domestica (domestic pig)
C/Date: 19-May-1994 #sequence_revision 19-May-1994 #text_change 09-Jul-2004
C/Accession: JN0900; S36822; S34586
R/Storici, P.; Zanetti, M.
Biochem. Biophys. Res. Commun. 196, 1363-1368, 1993
A/Title: A novel cDNA sequence encoding a pig leukocyte antimicrobial peptide with a cat
A/Reference number: JN0900; MUID:94071898; PMID:8250892
```

```
A/Accession: JN0900
A/Molecule type: mRNA
A/Residues: 1-147 <STO>
A/Cross-references: UNIPROT:P32195; UNIPARC:UPI0000131776; GB:L24745; NID:g431435; PIDN:
R/Mirgorodskaya, O.A.; Shevchenko, A.A.; Abdalla, K.O.M.A.; Chernushevich, I.V.; Egorov,
FEBS Lett. 330, 339-342, 1993
A/Title: Primary structure of three cationic peptides from porcine neutrophils. Sequence
A/Reference number: S36820; MUID:93387466; PMID:8375505
A/Accession: S36822
A/Molecule type: protein
A/Residues: 131-146 <MIR>
A/Cross-references: UNIPARC:UPI000014310F
R/Kokryakov, V.N.; Harwig, S.S.L.; Panyutich, E.A.; Shevchenko, A.A.; Alekhina, G.M.; Sha
FEBS Lett. 327, 231-236, 1993
A/Title: Protegrins: leukocyte antimicrobial peptides that combine features of corticost
A/Reference number: S34585; MUID:93327946; PMID:8335113
A/Accession: S34586
A/Molecule type: protein
A/Residues: 131-146 <KOK>
A/Cross-references: UNIPARC:UPI000014310F
C/Comment: This protein plays a role in the nonoxidative antimicrobial defense mechanism
C/Superfamily: cathelin; cystatin homology
C/Keywords: amidated carboxyl end; antibacterial; neutrophil
F/1-29/Domain: signal sequence #status predicted <SIG>
F/22-129/Domain: cystatin homology <CYS>
F/131-146/Product: protegrin 2 #status experimental <MAT>
F/146/Modified site: amidated carboxyl end (Val) (amide in mature form from following gl
Query Match 60.4%; Score 55; DB 2; Length 147;
Best Local Similarity 64.7%; Pred. No. 0.086;
Matches 11; Conservative 0; Mismatches 6; Indels 0; Gaps 0;

QY 1 RGGRLSYRRRFTSTG 17
Db 131 RGGRLCYRRRFCVCG 147

RESULT 3
A53895
  protegrin 3 precursor - pig
N/Alternate names: neutrophil peptide 2
C/Species: Sus scrofa domestica (domestic pig)
C/Date: 01-Dec-1995 #sequence_revision 01-Dec-1995 #text_change 09-Jul-2004
C/Accession: S66285; A53895; S34587; S36821; S57608
R/Zhao, C.; Ganz, T.; Lehrer, R.I.
FEBS Lett. 368, 197-202, 1995
A/Title: The structure of porcine protegrin genes.
A/Reference number: S66283; MUID:95354835; PMID:7628604
A/Accession: S66285
A/Molecule type: DNA
A/Residues: 1-149 <ZH3>
A/Cross-references: UNIPROT:P32196; UNIPARC:UPI0000131777; EMBL:X84095; NID:g887644; PID:
R/Zhao, C.; Liu, L.; Lehrer, R.I.
FEBS Lett. 346, 285-288, 1994
A/Title: Identification of a new member of the protegrin family by cDNA cloning.
A/Reference number: S45712; MUID:94283613; PMID:8013647
A/Accession: A53895
A/Status: not compared with conceptual translation
A/Molecule type: mRNA
A/Residues: 1-149 <ZHA>
A/Cross-references: UNIPARC:UPI0000131777; GB:X83267; NID:g603037; PIDN:CAAS8240.1; PID:
R/Kokryakov, V.N.; Harwig, S.S.L.; Panyutich, E.A.; Shevchenko, A.A.; Alekhina, G.M.; Sha
FEBS Lett. 327, 231-236, 1993
A/Title: Protegrins: leukocyte antimicrobial peptides that combine features of corticost
A/Reference number: S34585; MUID:93327946; PMID:8335113
A/Accession: S34587
A/Molecule type: protein
A/Residues: 131-148 <KOK>
A/Cross-references: UNIPARC:UPI0000143110
R/Mirgorodskaya, O.A.; Shevchenko, A.A.; Abdalla, K.O.M.A.; Chernushevich, I.V.; Egorov,
FEBS Lett. 330, 339-342, 1993
A/Title: Primary structure of three cationic peptides from porcine neutrophils. Sequence
A/Reference number: S36820; MUID:93387466; PMID:8375505
```

A;Cross-references: UNIPROT:Q86541; UNIPARC:UPI00000F9P61; GB:S45593; NID:G256417; PIDN:  
C;Note: sequence extracted from NCBI backbone (NCBIN:114637, NCBIP:114639)  
C;Superfamily: potato virus nucleic acid-binding protein  
C;Keywords: DNA binding; zinc finger  
F;55-75/Region: zinc finger

Query Match 51.6%; Score 47; DB 1; Length 94;  
Best Local Similarity 52.9%; Pred. No. 1.2;  
Matches 9; Conservative 4; Mismatches 4; Indels 0; Gaps 0;

QY 2 GGRLSYRRRFFSTGTG 18  
|||:|:|:|  
DB 38 GGRSTYARKRRARSIGR 54

RESULT 6  
S53982  
hypothetical protein 447 - actinophaga RP3  
C;Species: actinophaga RP3  
C;Date: 28-Oct-1996 #sequence\_revision 13-Mar-1997 #text\_change 13-Mar-1997  
R;Accession: S53982  
R;Gabriel, K.; Schmid, H.; Schmidt, U.; Rausch, H.  
Nucleic Acids Res. 23, 58-63, 1995  
A;Title: The actinophaga RP3 DNA integrates site-specifically into the putative tRNA(Arg  
A;Reference number: S53981; MUID:95175370; PMID:7870591  
A;Accession: S53982  
A;Status: preliminary  
A;Molecule type: DNA  
A;Residues: 1-447 <GAB>  
A;Cross-references: UNIPARC:UPI000017A848; EMBL:X80661  
C;Genetics:  
A;Start codon: GTG

Query Match 51.6%; Score 47; DB 2; Length 447;  
Best Local Similarity 47.1%; Pred. No. 5.3;  
Matches 8; Conservative 5; Mismatches 4; Indels 0; Gaps 0;

QY 1 RGGRLSYRRRFFSTGTG 17  
|||:|:|:|  
DB 9 RGGSVAYAEKRVSTAKG 25

RESULT 7  
T32047  
hypothetical protein K07E8.3 - Caenorhabditis elegans  
C;Species: Caenorhabditis elegans  
C;Date: 29-Oct-1999 #sequence\_revision 29-Oct-1999 #text\_change 09-Jul-2004  
C;Accession: T32047  
R;Jones, K.; Kramer, J.  
submitted to the EMBL Data Library, July 1997  
A;Description: The sequence of C. elegans cosmid K07E8.  
A;Reference number: Z21116  
A;Accession: T32047  
A;Status: preliminary; translated from GB/EMBL/DBD  
A;Molecule type: DNA  
A;Residues: 1-231 <JON>  
A;Cross-references: UNIPROT:O16689; UNIPARC:UPI000017BA9F; EMBL:AF016678; PIDN:AAB66149.1  
A;Experimental source: strain Bristol N2; clone K07E8  
C;Genetics:  
A;Gene: CESP:K07E8.3  
A;Map position: 2  
A;Introns: 69/3; 104/1; 171/3; 203/3

Query Match 50.5%; Score 46; DB 2; Length 231;  
Best Local Similarity 47.1%; Pred. No. 4.1;  
Matches 8; Conservative 3; Mismatches 6; Indels 0; Gaps 0;

QY 1 RGGRLSYRRRFFSTGTG 17  
|||:|:|:|  
DB 74 RGGVDYHDKRYPNRTG 90

RESULT 8

QOAG6T  
hypothetical protein 6 - Agrobacterium tumefaciens plasmids  
C:Species: Agrobacterium tumefaciens  
C>Date: 13-Aug-1986 #sequence\_revision 13-Aug-1986 #text\_change 09-Jul-2004  
C:Accession: A04498; S28691  
R:Giesen, J.; De Beuckeleer, M.; Seurinck, J.; Deboeck, P.; De Greve, H.; Lemmers, M.; VEMBO J. 3, 835-846, 1984  
A:Title: The complete nucleotide sequence of the TL-DNA of the Agrobacterium tumefaciens  
A:Reference number: A91001; MUID:84207942; PMID:6327292  
A:Accession: A04498  
A:Molecule type: DNA  
A:Residues: 1-191 <GIE>  
A:Cross-references: UNIPROT:P04030; UNIPARC:UPI00000008AB; GB:X00493; GB:J05108; GB:X002  
A:Experimental source: plasmid pRIach5  
R:Barker, R.F.; Idler, K.B.; Thompson, D.V.; Kemp, J.D.  
Plant Mol. Biol. 2, 335-350, 1983  
A:Title: Nucleotide sequence of the T-DNA region from the Agrobacterium tumefaciens octo  
A:Reference number: S28683  
A:Accession: S28691  
A>Status: translation not shown  
A:Molecule type: DNA  
A:Residues: 1-191 <BAR>  
A:Cross-references: UNIPARC:UPI00000008AB; EMBL:X00493; NID:g39062; PIDN:CAA25171.1; PID  
A:Experimental source: plasmid pTI15955  
C:Genetics:  
A:Genome: plasmid  
C:Superfamily: T-6b protein  
C:Keywords: crown gall tumor

Query Match 49.5%; Score 45; DB 1; Length 191;  
Best Local Similarity 50.0%; Pred. No. 5.1;  
Matches 7; Conservative 5; Mismatches 2; Indels 0; Gaps 0;

QY 2 GGRLSYSRRRFFSTS 15  
|||:|:|:|:|:  
Db 112 GGRINYSKNEYSSS 125

RESULT 9  
A30832  
hypothetical protein 6a - Agrobacterium tumefaciens plasmid pTI737  
C:Species: Agrobacterium tumefaciens  
C>Date: 30-Jun-1989 #sequence\_revision 30-Jun-1989 #text\_change 09-Jul-2004  
C:Accession: A30832  
R:Vanderleyden, J.; Desair, J.; De Meirman, C.; Michiels, K.; Van Gool, A.; Jen, G.; Ch  
Plant Mol. Biol. 7, 33-41, 1986  
A:Title: Nucleotide sequence of the T-DNA region encoding transcripts 6a and 6b of the p  
A:Reference number: A93763  
A:Accession: A30832  
A:Molecule type: DNA  
A:Residues: 1-186 <VAN>  
A:Cross-references: UNIPROT:Q52604; UNIPARC:UPI000000B68A2  
C:Genetics:  
A:Genome: plasmid  
C:Superfamily: T-6b protein

Query Match 48.4%; Score 44; DB 2; Length 186;  
Best Local Similarity 57.1%; Pred. No. 7.2;  
Matches 8; Conservative 3; Mismatches 3; Indels 0; Gaps 0;

QY 2 GGRLSYSRRRFFSTS 15  
|||:|:|:|:|:  
Db 107 GGRINYSRNEHSSS 120

RESULT 10  
AC3229  
protein 6a [imported] - Agrobacterium tumefaciens (strain C58, Dupont) plasmid Ti  
C:Species: Agrobacterium tumefaciens  
C>Date: 11-Jan-2002 #sequence\_revision 11-Jan-2002 #text\_change 09-Jul-2004  
C:Accession: AC3229  
R:Wood, D.W.; Secubal, J.C.; Kaul, R.; Monke, D.; Chen, L.; Wood, G.E.; Chen, Y.; Woo, H  
erage, G.; Gillet, W.; Grant, C.; Guenther, D.; Kuttyavin, T.; Levy, R.; Li, M.; McClell

; Karp, P.; Romero, P.; Zhang, S.  
Science 294, 2317-2323, 2001  
A:Authors: Yoo, H.; Tao, Y.; Biddle, P.; Jung, M.; Krespan, W.; Perry, M.; Gordon-Kamm, I  
ster, E.W.  
A:Title: The Genome of the Natural Genetic Engineer Agrobacterium tumefaciens C58.  
A:Reference number: AB2577; MUID:21608550; PMID:11743193  
A:Accession: AC3229  
A>Status: preliminary  
A:Molecule type: DNA  
A:Residues: 1-186 <KUR>  
A:Cross-references: UNIPROT:Q9R430; UNIPARC:UPI00000D609F; GB:AE008690; PIDN:AAL46249.1;  
A:Experimental source: strain C58 (Dupont)  
C:Genetics:  
A:Gene: gene6a  
A:Genome: plasmid  
C:Superfamily: T-6b protein

Query Match 48.4%; Score 44; DB 2; Length 186;  
Best Local Similarity 57.1%; Pred. No. 7.2;  
Matches 8; Conservative 3; Mismatches 3; Indels 0; Gaps 0;

QY 2 GGRLSYSRRRFFSTS 15  
|||:|:|:|:|:  
Db 107 GGRINYSRNEHSSS 120

RESULT 11  
DB1896  
Neisseria meningitidis hypothetical protein NMA1282 - Neisseria meningitidis (strain Z249  
C:Species: Neisseria meningitidis  
C>Date: 05-May-2000 #sequence\_revision 05-May-2000 #text\_change 09-Jul-2004  
C:Accession: DB1896  
R:Parkhill, J.; Achtman, M.; James, K.D.; Bentley, S.D.; Churcher, C.; Klee, S.R.; Morel  
; Holroyd, S.; Jagels, K.; Leather, S.; Moule, S.; Mungall, K.; Quail, M.A.; Rajandream,  
Nature 404, 502-506, 2000  
A:Title: Complete DNA sequence of a serogroup A strain of Neisseria meningitidis Z2491.  
A:Reference number: A81775; MUID:20222556; PMID:10761919  
A:Accession: DB1896  
A>Status: preliminary  
A:Molecule type: DNA  
A:Residues: 1-293 <PAR>  
A:Cross-references: UNIPROT:Q9JUJ7; UNIPARC:UPI00000C4B6C; GB:AL162755; GB:AL157959; NID:  
A:Experimental source: serogroup A, strain Z2491  
C:Genetics:  
A:Gene: NMA1282  
C:Superfamily: Neisseria meningitidis hypothetical protein NMA1282

Query Match 48.4%; Score 44; DB 2; Length 293;  
Best Local Similarity 57.1%; Pred. No. 11;  
Matches 8; Conservative 2; Mismatches 4; Indels 0; Gaps 0;

QY 4 RLSYSRRRFFSTGTG 17  
|||:|:|:|:|:  
Db 38 RLGSYRKNFPEQTG 51

RESULT 12  
T03240  
FLO/LFY protein homolog NFL1 - common tobacco  
C:Species: Nicotiana tabacum (common tobacco)  
C>Date: 24-Mar-1999 #sequence\_revision 24-Mar-1999 #text\_change 09-Jul-2004  
C:Accession: T03240  
R:Kelly, A.J.; Bonlander, M.B.; Meeks-Wagner, D.R.  
Plant Cell 7, 225-234, 1995  
A:Title: NFL, the tobacco homologue of FLORICAULA and LEAFY, is transcriptionally expres  
A:Reference number: Z14855; MUID:95276463; PMID:7756832  
A:Accession: T03240  
A>Status: preliminary; translated from GB/EMBL/DBJ  
A:Molecule type: DNA  
A:Residues: 1-413 <KEL>  
A:Cross-references: UNIPROT:Q40504; UNIPARC:UPI000012A83A; EMBL:U16172; NID:9561681; PIDN  
A:Experimental source: cultivar Sameun  
C:Genetics:

A;Introns: 154/1; 288/3  
C;Superfamily: Arabidopsis thaliana LFY floral meristem identity control protein  
C;Keywords: transcription regulation

Query Match 48.4%; Score 44; DB 2; Length 413;  
Best Local Similarity 52.9%; Pred. No. 15;  
Matches 9; Conservative 2; Mismatches 6; Indels 0; Gaps 0;

Qy 2 GGRLSYSRRRPFSTGTGR 18  
|||: ||: |||||  
Db 186 GGRMKQRKKKVVSTGR 202

RESULT 13  
B89978  
glutamyl-tRNAglut amidotransferase subunit B [imported] - Staphylococcus aureus (strain N  
C;Species: Staphylococcus aureus  
C;Date: 10-May-2001 #sequence\_revision 10-May-2001 #text\_change 09-Jul-2004  
C;Accession: B89978  
R;Kuroda, M.; Ohca, T.; Uchiyama, I.; Baba, T.; Yuzawa, H.; Kobayashi, I.; Cui, L.; Ogino  
ma, A.; Mizutani-Ui, Y.; Kobayashi, N.; Sawano, T.; Inoue, R.; Kaito, C.; Sekimizu, K.;  
C.; Shiba, T.; Hattori, M.; Ogasawara, N.; Hayashi, H.; Hiramatsu, K.  
Lancet 357, 1225-1240, 2001  
A;Title: Whole genome sequencing of methicillin-resistant Staphylococcus aureus.  
A;Reference number: A89758; MUID:21311952; PMID:11418146  
A;Accession: B89978  
A;Status: preliminary  
A;Molecule type: DNA  
A;Residues: 1-475 <KUR>  
A;Cross-references: UNIPROT:Q9SV7; UNIPARC:UPI000012B162; GB:BA000018; PID:g13701692; F  
A;Experimental source: strain N315  
C;Genetics:  
A;Gene: SA1715  
C;Superfamily: PET112 protein

Query Match 48.4%; Score 44; DB 2; Length 475;  
Best Local Similarity 47.1%; Pred. No. 18;  
Matches 8; Conservative 2; Mismatches 7; Indels 0; Gaps 0;

Qy 2 GGRLSYSRRRPFSTGTGR 18  
|||: |||: |||:  
Db 238 GGEIGQETRRPFDESTGK 254

RESULT 14  
H72730  
probable acyl-CoA dehydrogenase, short-chain specific APE0385 - Aeropyrum pernix (strain  
C;Species: Aeropyrum pernix  
C;Date: 20-Aug-1999 #sequence\_revision 20-Aug-1999 #text\_change 09-Jul-2004  
C;Accession: H72730  
R;Kawarabayashi, Y.; Hino, Y.; Horikawa, H.; Yamazaki, S.; Haikawa, Y.; Jin-no, K.; Takah  
awa, H.; Takamiya, M.; Masuda, S.; Funahashi, T.; Tanaka, T.; Kudoh, Y.; Yamazaki, J.; K  
DNA Res. 6, 83-101, 1999  
A;Title: Complete genome sequence of an aerobic hyper-thermophilic Crenarchaeon, Aeropyr  
A;Reference number: A72450; MUID:99310339; PMID:10382966  
A;Accession: H72730  
A;Status: preliminary  
A;Molecule type: DNA  
A;Residues: 1-532 <KAW>  
A;Cross-references: UNIPROT:Q9YF56; UNIPARC:UPI000005DB09; DDBJ:AP0000059; NID:g5103911;  
A;Experimental source: strain K1  
C;Genetics:  
A;Gene: APE0385

Query Match 48.4%; Score 44; DB 2; Length 532;  
Best Local Similarity 52.9%; Pred. No. 20;  
Matches 9; Conservative 2; Mismatches 6; Indels 0; Gaps 0;

Qy 1 RGGRLSYRRRPFSTGTG 17  
|||: |||: |||:  
Db 222 RGGGLNYSVRLKDKSG 238

## RESULT 15

JQ1251  
hypothetical 12.6K protein - chrysanthemum virus B  
C;Species: chrysanthemum virus B  
C;Date: 30-Sep-1993 #sequence\_revision 30-Sep-1993 #text\_change 09-Jul-2004  
C;Accession: JQ1251

R;Levay, K.; Zavrjev, S.  
J. Gen. Virol. 72, 2333-2337, 1991  
A;Title: Nucleotide sequence and gene organization of the 3'-terminal region of chrysant.  
A;Reference number: JQ1246; MUID:92013948; PMID:1919520  
A;Accession: JQ1251

A;Molecule type: genomic RNA  
A;Residues: 1-107 <LEV>

A;Cross-references: UNIPROT:P37992; UNIPARC:UPI0000138A0A; GB:S60150; NID:g237315; PIDN:  
C;Superfamily: potato virus nucleic acid-binding protein

Query Match 47.3%; Score 43; DB 2; Length 107;  
Best Local Similarity 56.2%; Pred. No. 6.3;  
Matches 9; Conservative 2; Mismatches 5; Indels 0; Gaps 0;

Qy 3 GRLSYSRRRPFSTGTGR 18  
|||: |||: |||:  
Db 40 GRSSVARRRREALGLR 55

RESULT 16  
WMVYVP5

nucleic acid-binding protein - potato virus M (strain Russian)  
C;Species: potato virus M  
A;Note: host Lycopersicon esculentum (tomato)  
C;Date: 31-Mar-1990 #sequence\_revision 23-Mar-1995 #text\_change 09-Jul-2004  
C;Accession: F54333; PNO006; PNO095; S21606

R;Zavrjev, S.K.; Kanyuka, K.V.; Levay, K.E.  
J. Gen. Virol. 72, 9-14, 1991

A;Title: The genome organization of potato virus M RNA.  
A;Reference number: A54333; MUID:91116326; PMID:1990070  
A;Accession: F54333

A;Molecule type: genomic RNA  
A;Residues: 1-108 <ZAV>

R;Rupasov, V.V.; Morozov, S.Y.; Kanyuka, K.V.; Zavrjev, S.K.  
J. Gen. Virol. 70, 1861-1869, 1989

A;Title: Partial nucleotide sequence of potato virus M RNA shows similarities to potexvi  
A;Reference number: A92800; MUID:89293091; PMID:2738581  
A;Accession: PNO006

A;Molecule type: mRNA  
A;Residues: 1-79, 'LVSLTWCARNLLMKE' <RUP>  
A;Cross-references: UNIPARC:UPI0000174B3D  
A;Note: this sequence has been corrected  
R;Zavrjev, S.K.; Kanyuka, K.V.; Levay, K.E.  
Mol. Biol. (Mosk.) 25, 761-769, 1991

A;Title: The complete nucleotide sequence of potato virus M genomic RNA.  
A;Reference number: PNO093; MUID:92049299; PMID:1944258  
A;Accession: PNO095

A;Molecule type: Genomic RNA  
A;Residues: 1-108 <ZA2>  
A;Cross-references: UNIPARC:UPI0000138A0F; GB:X53062; NID:g61291; PID:g  
A;Note: this is a revision to the sequence from reference A92800  
R;Zavrjev, S.K.

submitted to the EMBL Data Library, May 1990  
A;Reference number: S21601  
A;Accession: S21606

A;Status: preliminary  
A;Molecule type: genomic RNA  
A;Residues: 1-79, 'LVSLTWCARNLLMKE' <ZA3>  
A;Cross-references: UNIPARC:UPI0000174B3D; EMBL:X53062

A;Experimental source: Russian wild type  
C;Superfamily: potato virus nucleic acid-binding protein  
C;Keywords: DNA binding; metal binding; nucleotide binding; zinc finger  
P;57-78/Region: zinc finger

Query Match 47.3%; Score 43; DB 1; Length 108;  
Best Local Similarity 52.9%; Pred. No. 6.3;

```
Matches 9; Conservative 2; Mismatches 6; Indels 0; Gaps 0;

QY 2 GGRLSYRRRFRSTGTGR 18
    ||| |::|||:|
Db 40 GGRSKYARRRAISAR 56

RESULT 17
S12976
12K protein - potato virus M
C:Species: potato virus M
C>Date: 19-Mar-1997 #sequence_revision 19-Mar-1997 #text_change 09-Jul-2004
C:Accession: S12976
R:Gramstat, A.; Courtbozanis, A.; Rohde, W.
FEBS Lett. 276, 34-38, 1990
A:Title: The 12 kDa protein of potato virus M displays properties of a nucleic acid-binding protein
A:Reference number: S12975; MUID:91092429; PMID:2265707
A:Accession: S12976
A>Status: preliminary
A:Molecule type: genomic RNA
A:Residues: 1-108 <GRA>
A:Cross-references: UNIPROT:Q01687; UNIPARC:UPI0000138A0E; GB:X57440; NID:G61400; PIDN:CAC89500.1;
C:Superfamily: potato virus nucleic acid-binding protein

Query Match 47.3%; Score 43; DB 2; Length 108;
Best Local Similarity 52.9%; Pred. No. 6.3;
Matches 9; Conservative 2; Mismatches 6; Indels 0; Gaps 0;

QY 2 GGRLSYRRRFRSTGTGR 18
    ||| |::|||:|
Db 40 GGRSKYARRRAISAR 56

RESULT 18
AI0079
probable glycoproteinase gcp [imported] - Yersinia pestis (strain CO92)
C:Species: Yersinia pestis
C>Date: 02-Nov-2001 #sequence_revision 02-Nov-2001 #text_change 09-Nov-2001
C:Accession: AI0079
R:Parkhill, J.; Wren, B.W.; Thomson, N.R.; Titball, R.W.; Holden, M.T.G.; Prentice, M.B.;
deno-Tarraga, A.M.; Chillingworth, T.; Cronin, A.; Davies, R.M.; Davis, P.; Dougan, G.;
il, M.; Rutherford, K.; Simmonds, M.; Skelton, J.; Stevens, K.; Whitehead, S.; Barrell,
Nature 413, 523-527, 2001
A:Title: Genome sequence of Yersinia pestis, the causative agent of plague.
A:Reference number: AB0001; MUID:21470413; PMID:11586360
A:Accession: AI0079
A>Status: preliminary
A:Molecule type: DNA
A:Residues: 1-337 <KUR>
A:Cross-references: UNIPARC:UPI00000CD702; GB:AL590842; PIDN:CAC89500.1; PID:G15978736;
C:Genetics:
A:Gene: gcp
C:Superfamily: O-sialoglycoprotein endopeptidase

Query Match 47.3%; Score 43; DB 2; Length 337;
Best Local Similarity 47.1%; Pred. No. 19;
Matches 8; Conservative 2; Mismatches 7; Indels 0; Gaps 0;

QY 1 RGGRLSYRRRFRSTGTG 17
    ||| |::|||:|
Db 286 RGGEVFYARPEFCTDNG 302

RESULT 19
C72642
hypothetical protein APE0571 - Aeropyrum pernix (strain K1)
C:Species: Aeropyrum pernix
C>Date: 20-Aug-1999 #sequence_revision 20-Aug-1999 #text_change 09-Jul-2004
C:Accession: C72642
R:Kawarabayashi, Y.; Hino, Y.; Horikawa, H.; Yamazaki, S.; Haikawa, Y.; Jin-no, K.; Takah
awa, H.; Takamiya, M.; Masuda, S.; Funahashi, T.; Tanaka, T.; Kudoh, Y.; Yamazaki, J.; K
DNA Res. 6, 83-101, 1999
A:Title: Complete genome sequence of an aerobic hyper-thermophilic Crenarchaeon, Aeropyru
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A:Reference number: A72450; MUID:99310339; PMID:10382966
A:Accession: C72642
A>Status: preliminary
A:Molecule type: DNA
A:Residues: 1-118 <KAW>
A:Cross-references: UNIPROT:Q9YBK7; UNIPARC:UPI000005DBD0; DDBJ:AF000060; NID:G5104188;
C:Genetics:
A:Gene: APE0571

Query Match 46.2%; Score 42; DB 2; Length 118;
Best Local Similarity 81.8%; Pred. No. 10;
Matches 9; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1 RGGRLSYRRR 11
    ||| |::|||:|
Db 21 RGGRLSSRRR 31

RESULT 20
AB3420
hypothetical phage protein BME11344 [imported] - Brucella melitensis (strain 16M)
C:Species: Brucella melitensis
C>Date: 01-Feb-2002 #sequence_revision 01-Feb-2002 #text_change 09-Jul-2004
C:Accession: AB3420
R:DelVecchio, V.G.; Kapatral, V.; Redkar, R.J.; Patra, G.; Mijer, C.; Los, T.; Ivanova, I.;
; Mazur, M.; Goltzman, E.; Selkov, E.; Eizer, P.H.; Hagius, S.; O'Callaghan, D.; Letess
Proc. Natl. Acad. Sci. U.S.A. 99, 443-448, 2002
A:Title: The genome sequence of the facultative intracellular pathogen Brucella melitensis
A:Reference number: AB3252; PMID:11756688
A:Accession: AB3420
A>Status: preliminary
A:Molecule type: DNA
A:Residues: 1-210 <KUR>
A:Cross-references: UNIPROT:Q8YGL8; UNIPROT:Q8G1V4; UNIPARC:UPI0000058029; GB:AB008917;
A:Experimental source: strain 16M
C:Genetics:
A:Gene: BME11344
A:Map position: 1

Query Match 46.2%; Score 42; DB 2; Length 210;
Best Local Similarity 47.1%; Pred. No. 17;
Matches 8; Conservative 2; Mismatches 7; Indels 0; Gaps 0;

QY 1 RGGRLSYRRRFRSTGTG 17
    ||| |::|||:|
Db 38 RNARWAHSRRHFDAGTG 54

RESULT 21
A41950
retrovirus-related hypothetical protein 1 - Trypanosoma cruzi retrotransposon
C:Species: Trypanosoma cruzi
C>Date: 04-Mar-1993 #sequence_revision 18-Nov-1994 #text_change 08-Jan-1999
C:Accession: A41950
R:Villanueva, M.S.; Williams, S.P.; Beard, C.B.; Richards, F.F.; Aksoy, S.
Mol. Cell. Biol. 11, 6139-6148, 1991
A:Title: A new member of a family of site-specific retrotransposons is present in the spi
A:Reference number: A41950; MUID:92049344; PMID:1719380
A:Accession: A41950
A>Status: preliminary
A:Molecule type: DNA
A:Residues: 1-386 <VIL>
A:Cross-references: UNIPARC:UPI000011DB57; GB:M62862; NID:G162247; PID:G162248
A:Note: sequence extracted from NCBI backbone (NCBIN:66378, NCBIP:66379)

Query Match 46.2%; Score 42; DB 2; Length 386;
Best Local Similarity 44.4%; Pred. No. 31;
Matches 8; Conservative 4; Mismatches 6; Indels 0; Gaps 0;

QY 1 RGGRLSYRRRFRSTGTGR 18
    ||| |::|||:|
Db 153 KGGRAGVATRRFSGTTNQ 170
```





C;Accession: T38308; T38381  
R;Skelton, J.; Churcher, C.M.; Barrell, B.G.; Rajandream, M.A.; Walsh, S.V.; Wood, V.  
submitted to the EMBL Data Library, September 1997  
A;Reference number: Z21785  
A;Accession: T38308  
A;Molecule type: DNA  
A;Residues: 1-325 <SKE>  
A;Cross-references: UNIPROT:P78890; UNIPARC:UPI000006C8C6; EMBL:Z99163; PIDN:CAB16245.1;  
A;Experimental source: strain 972h-; cosmid c23H3  
R;Devlin, K.; Churcher, C.M.; Barrell, B.G.; Rajandream, M.A.; Wood, V.  
submitted to the EMBL Data Library, August 1997  
A;Reference number: Z21737  
A;Accession: T38381  
A;Molecule type: DNA  
A;Residues: 1-87 <DEV>  
A;Cross-references: UNIPARC:UPI0000169022; EMBL:Z98944; PIDN:CAB11598.1; GSPDB:GN000066;  
A;Experimental source: strain 972h-; cosmid c25H1  
C;Genetics:  
A;Gene: SPAC23H3.15c; SPDB:SPAC25H1.01c  
A;Map position: 1

Query Match 45.1%; Score 41; DB 2; Length 325;  
Best Local Similarity 60.0%; Pred. No. 39;  
Matches 9; Conservative 1; Mismatches 5; Indels 0; Gaps 0;

QY 1 RGRLSYSRRRSTG 15  
||| ||||| :||  
Db 96 RGGDTYSRRHDDSS 110

RESULT 28  
AC2761  
penicillin binding protein [imported] - Agrobacterium tumefaciens (strain C58, Dupont)  
C;Species: Agrobacterium tumefaciens  
C;Date: 11-Jan-2002 #sequence\_revision 11-Jan-2002 #text\_change 09-Jul-2004  
C;Accession: AC2761  
R;Wood, D.W.; Setubal, J.C.; Kaul, R.; Monks, D.; Chen, L.; Wood, G.E.; Chen, Y.; Woo, I.  
erage, G.; Gillet, W.; Grant, C.; Guenther, D.; Kutayin, T.; Levy, R.; Li, M.; McClellan  
; Karp, P.; Romero, P.; Zhang, S.  
Science 294, 2317-2323, 2001  
A;Authors: Yoo, H.; Tao, Y.; Biddle, P.; Jung, M.; Krespan, W.; Perry, M.; Gordon-Kamm,  
ster, E.W.  
A;Title: The Genome of the Natural Genetic Engineer Agrobacterium tumefaciens C58.  
A;Reference number: AB2577; MUID:21608550; PMID:11743193  
A;Accession: AC2761  
A;Status: preliminary  
A;Molecule type: DNA  
A;Residues: 1-390 <KUR>  
A;Cross-references: UNIPROT:Q8UF99; UNIPARC:UPI0000164602; GB:AE008688; PIDN:AAL42505.1;  
A;Experimental source: strain C58 (Dupont)  
C;Genetics:  
A;Gene: dac  
A;Map position: circular chromosome

Query Match 45.1%; Score 41; DB 2; Length 390;  
Best Local Similarity 52.9%; Pred. No. 46;  
Matches 9; Conservative 1; Mismatches 7; Indels 0; Gaps 0;

QY 1 RGRLSYSRRRSTG 17  
||| ||||| :|||  
Db 155 RAGELGMRNRSIFSSTG 171

RESULT 29  
A97542  
D-ala-D-ala-carboxypeptidase (PA3999) [imported] - Agrobacterium tumefaciens (strain C58)  
C;Species: Agrobacterium tumefaciens  
C;Date: 30-Sep-2001 #sequence\_revision 30-Sep-2001 #text\_change 09-Jul-2004  
C;Accession: A97542  
R;Goodner, B.; Hinkle, G.; Gattung, S.; Miller, N.; Blanchard, M.; Quorollo, B.; Goldman,  
A.; Liu, F.; Wollam, C.; Allinger, M.; Doughty, D.; Scott, C.; Lappas, C.; Markelz, B.;  
Science 294, 2323-2328, 2001  
A;Title: Genome Sequence of the Plant Pathogen and Biotechnology Agent Agrobacterium tum

A;Reference number: A97359; MUID:21608551; PMID:11743194  
A;Accession: A97542  
A;Status: preliminary  
A;Molecule type: DNA  
A;Residues: 1-413 <KUR>  
A;Cross-references: UNIPROT:Q8UF99; UNIPARC:UPI00000D1B95; GB:AE007869; PIDN:AAK87290.1;  
C;Genetics:  
A;Gene: AGR\_C\_2763  
A;Map position: circular chromosome

Query Match 45.1%; Score 41; DB 2; Length 413;  
Best Local Similarity 52.9%; Pred. No. 48;  
Matches 9; Conservative 1; Mismatches 7; Indels 0; Gaps 0;

QY 1 RGRLSYSRRRSTG 17  
||| ||||| :|||  
Db 178 RAGELGMRNRSIFSSTG 194

RESULT 30  
S53920  
SNG1 protein - yeast (Saccharomyces cerevisiae)  
N;Alternate names: protein G4883; protein G7591; protein YGR197c  
C;Species: Saccharomyces cerevisiae  
C;Date: 08-Jul-1995 #sequence\_revision 01-Sep-1995 #text\_change 09-Jul-2004  
C;Accession: S53920; S53895; S59182; S64515; S64519  
R;Nombela, C.  
submitted to the EMBL Data Library, November 1994  
A;Reference number: S53918  
A;Accession: S53920  
A;Molecule type: DNA  
A;Residues: 1-547 <NOM>  
A;Cross-references: UNIPROT:P46950; UNIPARC:UPI000004F91B; EMBL:X82775; NID:g791126; PID:  
R;Grey, M.  
submitted to the EMBL Data Library, September 1993  
A;Reference number: S53895  
A;Accession: S53895  
A;Molecule type: DNA  
A;Residues: 1-116, 'V', 118-547 <GRE>  
A;Cross-references: UNIPARC:UPI000016883D; EMBL:X74920; NID:g7633390; PID:g7633391  
R;Guerrero, P.; Silva, A.M.E.; Barreiro, T.; Arroyo, J.; Garcia-Gonzalez, M.; Garcia-Sa-  
Yeast 11, 1087-1091, 1995  
A;Title: The complete sequence of a 9000 bp fragment of the right arm of Saccharomyces ce  
A;Reference number: S59180; MUID:96076633; PMID:7502584  
A;Accession: S59182  
A;Status: nucleic acid sequence not shown  
A;Molecule type: DNA  
A;Residues: 1-547 <GUE>  
A;Cross-references: UNIPARC:UPI000004F91B; EMBL:X82775; NID:g791126; PIDN:CAA58016.1; PII  
R;Arroyo, J.; Garcia-Gonzalez, M.; Garcia-Saez, M.I.; Sanchez-Perez, M.; Nombela, C.  
submitted to the Protein Sequence Database, May 1996  
A;Reference number: S64499  
A;Accession: S64515  
A;Molecule type: DNA  
A;Residues: 1-547 <ARR>  
A;Cross-references: UNIPARC:UPI000004F91B; EMBL:Z72982; NID:g1323350; PID:e243736; PID:g13  
A;Experimental source: strain S288C  
R;Guerrero, P.; Barreiro, T.; Cyrne, L.; Soares, H.; Maia e Silva, A.; Rodrigues-Pousa-  
submitted to the Protein Sequence Database, May 1996  
A;Reference number: S64517  
A;Accession: S64519  
A;Molecule type: DNA  
A;Residues: 1-547 <GUW>  
A;Cross-references: UNIPARC:UPI000004F91B; EMBL:Z72982; NID:g1323350; PID:e243736; PID:g13  
A;Experimental source: strain S288C  
C;Genetics:  
A;Gene: SGD:SGN1  
A;Cross-references: SGD:S0003429; MIPS:YGR197C  
A;Map position: 7R  
C;Superfamily: Saccharomyces cerevisiae hypothetical protein YOR015w  
C;Keywords: transmembrane protein  
F;110-126/Domain: transmembrane #status predicted <TM1>  
F;318-334/Domain: transmembrane #status predicted <TM2>

F.367-383/Domain: transmembrane #status predicted <TM3>  
F.417-433/Domain: transmembrane #status predicted <TM4>  
F.488-504/Domain: transmembrane #status predicted <TM5>

Query Match 45.1%; Score 41; DB 2; Length 547;  
Best Local Similarity 50.0%; Pred. No. 63;  
Matches 9; Conservative 4; Mismatches 3; Indels 2; Gaps 1;

Qy 2 GGR--LSYSRRRFFSTSTG 17  
|||:|:|:|:  
Db 26 GGRDGVSYSNQRFPAEGSG 43

**RESULT 31**

AC0884

glutathionylspermidine synthetase/amidase [imported] - Salmonella enterica subsp. enterica  
 A/Species: Salmonella enterica subsp. enterica serovar typhi  
 A/Note: this species has also been called Salmonella typhi  
 C/Date: 09-Nov-2001 #sequence\_revision 09-Nov-2001 #text\_change 18-Nov-2002  
 C/Accession: AC0984

R; Parkhill, J.; Dougan, G.; James, K.D.; Thomson, N.R.; Pickard, D.; Wain, J.; Churcher, T.; Connerton, P.; Cronin, A.; Davis, P.; Davies, R.M.; Dowd, L.; White, N.; Farrar, S.; Moule, S.; O'Gaora, P.  
Nature 413, 848-852, 2001

A:Authors: Parry, C.; Quail, M.; Rutherford, K.; Simmonds, M.; Stelton, J.; Stevens, K.;  
A:Title: Complete genome sequence of a multiple drug resistant *Salmonella enterica* serov  
A:Reference number: AB0502; MUID:21534947; PMID:11677608

**A;Accession: AC0884**

**A;Status: preliminary**

A;Molecule type: DNA

**A;Residues: 1-618. <PAR>**

A;Cross-references: UNIPARC:UPI000005A46A; GB:AL513382; PIDN:CAD02971.1; PID:ql6504219;

**C; Genetics:**

**A;Gene: STY3310**

Query Match	45.1%	Score 41;	DB 2;	Length 619;
Best Local Similarity	60.0%;	Pred. No. 71;		
Matches	9;	Conservative	1;	Mismatches
			5;	Indels
			0;	Gaps
			0;	Gaps

QY	4	RLSYRRRFFST	18
		:	
Db	301	RLSWORRRHHMIT	315

**RESULT 32**

A91113

glutathionylspermidine synthetase/amidase [imported] - Escherichia coli (strain O157:H7, C)  
Species: Escherichia coli  
C/Date: 18-Jul-2001 #sequence revision 18-Jul-2001 #text change 09-Jul-2004

C/Accession: A91113  
R/Researcher: T.; Makino, K.; Ohnishi, M.; Kurokawa, K.; Ishii, K.; Yokoyama, K.; Han, C.G.  
S/Subject: gasawara, N.; Yasunaga, T.; Kuhara, S.; Shiba, T.; Hattori, M.; Shinagawa, H.

DNA Res. 8, 11-22, 2001  
 A>Title: Complete genome sequence of enterohemorrhagic *Escherichia coli* O157:H7 and genomic  
 A,Reference number: A99629; PMID:21156231; PMID:11258796

**A;Accession: A91113**

**A;Status: preliminary**

**A;Molecule type: DNA**

A;Residues: 1-619 &lt;HAY&gt;

A; Cross-references: UNIPROT:Q8XBW3; UNIPARC:UPI00000D054F; GE:BA000007; PIDN:BA37296.1;  
A; Experimental source: strain O157:H7, substrain RMD 0509952

**C;Genetics:**

**A; Gene: EC83873**

Query Match	45.1%	Score 41; DB 2; Length 619;
Best Local Similarity	60.0%;	
Matches	9; Conservative	1; Mismatches
		5; Indels
		Gaps 0;

Qy 4 RLSYSRRRFFSTSTGR 18  
|||: ||| |||  
Db 302 RLSWORRRHHMITGR 316

RESULT 35

A56600

C;Species: Branchiostoma lanceolatum (common lancelet)

C;Date: 11-Aug-1995 #sequence\_revision 11-Aug-1995 #text\_change 09-Jul-2004

C;Accession: A56600; S24265  
R;Riener, D.; Dodemont, H.; Weber, K.  
Eur. J. Cell Biol. 58, 128-135, 1992  
A;Title: Analysis of the cDNA and gene encoding a cytoplasmic intermediate filament (IF) family.  
A;Reference number: A56600; MUID:92354564; PMID:1644059  
A;Accession: A56600  
A;Status: preliminary  
A;Molecule type: mRNA  
A;Residues: 1-464 <RIE>  
A;Cross-references: UNIPROT:Q04948; UNIPARC:UPI000012D3D5; EMBL:X64522; NID:g5724; PIDN:  
A;Note: sequence extracted from NCBI backbone (NCBIP:110465)  
A;Note: intron positions were also determined  
C;Superfamily: cytoskeletal keratin  
C;Keywords: cytosol; intermediate filament

Query Match 44.5%; Score 40.5; DB 2; Length 464;  
Best Local Similarity 61.1%; Pred. No. 66;  
Matches 11; Conservative 0; Mismatches 6; Indels 1; Gaps 1;

QY 2 GGRLSYSRR-RFSTSTGR 18  
||| ||| ||| ||| |||  
DB 25 GGRASYSSSGRFSGGGGR 42

RESULT 36  
ribosomal protein l31 [imported] - Caulobacter crescentus  
C;Species: Caulobacter crescentus  
C;Date: 20-Apr-2001 #sequence\_revision 20-Apr-2001 #text\_change 09-Jul-2004  
A;Accession: A87655  
R;Nierman, W.C.; Deiblyum, T.V.; Paulsen, I.T.; Nelson, K.E.; Eisen, J.; Heidelberg, J.  
B.; Laub, M.T.; Fejby, R.T.; Dodson, R.J.; Durkin, A.S.; Gwinn, M.L.; Haft, D.H.; Kolon  
n, J.; Ermolaeva, M.; White, O.; Salzberg, S.L.; Shapiro, L.; Venter, J.C.; Fraser, C.M.  
Proc. Natl. Acad. Sci. U.S.A. 98, 4136-4141, 2001  
A;Title: Complete Genome Sequence of Caulobacter crescentus.  
A;Reference number: A87249; MUID:21173698; PMID:11259647  
A;Accession: A87655  
A;Status: preliminary  
A;Molecule type: DNA  
A;Residues: 1-76 <STO>  
A;Cross-references: UNIPROT:Q9A3C9; UNIPARC:UPI0000133F04; GB:AE005673; NID:g13424965; H  
C;Genetics:  
A;Gene: CC3275

Query Match 44.0%; Score 40; DB 2; Length 76;  
Best Local Similarity 44.4%; Pred. No. 14;  
Matches 8; Conservative 4; Mismatches 6; Indels 0; Gaps 0;

QY 1 RGGRLSYRRRPFSTSTGR 18  
||| ||| ||| ||| |||  
DB 57 RGGRVSRFNAKFAFTGK 74

RESULT 37  
T33652  
hypothetical protein T06A10.2 - Caenorhabditis elegans  
C;Species: Caenorhabditis elegans  
C;Date: 29-Oct-1999 #sequence\_revision 29-Oct-1999 #text\_change 29-Oct-1999  
A;Accession: T33652  
R;Zhu, H.; Hinds, K.; Keppler, D.  
submitted to the EMBL Data Library, October 1998  
A;Description: The sequence of C. elegans cosmid T06A10.  
A;Reference number: Z21382  
A;Accession: T33652  
A;Status: preliminary; translated from GB/EMBL/DDBJ  
A;Molecule type: DNA  
A;Residues: 1-217 <ZHU>  
A;Cross-references: UNIPARC:UPI000017EB68; EMBL:AF099926; PIDN:AAC68906.1; GSFDB:GN00022  
A;Experimental source: strain Bristol N2; clone T06A10  
C;Genetics:  
A;Gene: CESP:T06A10.2  
A;Map position: 4

A;Introns: 30/3; 71/3; 105/3; 124/2; 172/1

Query Match 44.0%; Score 40; DB 2; Length 217;  
Best Local Similarity 57.1%; Pred. No. 39;  
Matches 8; Conservative 3; Mismatches 3; Indels 0; Gaps 0;

QY 5 LGSYSRRRPFSTSTGR 18  
||| ||| ||| ||| |||  
DB 105 ISFARFRVSVSTGR 118

RESULT 38  
D96597  
hypothetical protein TSA14.9 [imported] - Arabidopsis thaliana  
C;Species: Arabidopsis thaliana (mouse-ear cress)  
C;Date: 02-Mar-2001 #sequence\_revision 02-Mar-2001 #text\_change 12-Jul-2004  
A;Accession: D96597  
R;Theologis, A.; Ecker, J.R.; Palm, C.J.; Federspiel, N.A.; Kaul, S.; White, O.; Alonso,  
Chin, C.W.; Chung, M.K.; Conn, L.; Conway, A.B.; Conway, A.R.; Creasy, T.H.; Dewar, K.;  
ansen, N.P.; Hughes, B.; Huizar, L.  
Nature 408, 816-820, 2000  
A;Authors: Hunter, J.L.; Jenkins, J.; Johnson-Hopson, C.; Khan, S.; Khaykin, E.; Kim, C.;  
C.A.; Li, J.H.; Li, Y.; Lin, X.; Liu, S.X.; Liu, Z.A.; Luros, J.S.; Maiti, R.; Marziani,  
Rizzo, M.; Rooney, T.; Rowley, D.; Sakano, H.  
A;Authors: Salzberg, S.L.; Schwartz, J.R.; Shinn, P.; Southwick, A.M.; Sun, H.; Tallon, I.  
ker, M.; Wu, D.; Yu, G.; Fraser, C.M.; Venter, J.C.; Davis, R.W.  
A;Title: Sequence and analysis of chromosome 1 of the plant Arabidopsis.  
A;Reference number: A86141; MUID:21016719; PMID:11130712  
A;Accession: D96597  
A;Status: preliminary  
A;Molecule type: DNA  
A;Residues: 1-352 <STO>  
A;Cross-references: UNIPROT:Q9SAV3; UNIPARC:UPI00000A71A3; GB:AE005173; NID:g4204270; PII  
C;Genetics:  
A;Gene: TSA14.9  
A;Map position: 1  
C;Superfamily: pyruvate dehydrogenase, E1 component, beta subunit

Query Match 44.0%; Score 40; DB 2; Length 352;  
Best Local Similarity 57.1%; Pred. No. 61;  
Matches 8; Conservative 2; Mismatches 4; Indels 0; Gaps 0;

QY 5 LGSYSRRRPFSTSTGR 18  
||| ||| ||| ||| |||  
DB 17 LSHGARRVSTETGK 30

RESULT 39  
C85022  
hypothetical protein AT4g01730 [imported] - Arabidopsis thaliana  
C;Species: Arabidopsis thaliana (mouse-ear cress)  
C;Date: 16-Feb-2001 #sequence\_revision 16-Feb-2001 #text\_change 09-Jul-2004  
A;Accession: C85022  
R;anonymous, The European Union Arabidopsis Genome Sequencing Consortium, The Cold Spring  
Nature 402, 769-777, 1999  
A;Title: Sequence and analysis of chromosome 4 of the plant Arabidopsis thaliana.  
A;Reference number: A85001; MUID:20083488; PMID:10617198  
A;Accession: C85022  
A;Status: preliminary  
A;Molecule type: DNA  
A;Residues: 1-499 <STO>  
A;Cross-references: UNIPROT:Q9M115; UNIPARC:UPI000009EC49; GB:NC\_001268; NID:g7268216; P:  
C;Genetics:  
A;Gene: AT4g01730  
A;Map position: 4

Query Match 44.0%; Score 40; DB 2; Length 499;  
Best Local Similarity 64.3%; Pred. No. 85;  
Matches 9; Conservative 1; Mismatches 4; Indels 0; Gaps 0;

QY 3 GRLSYRRRPFSTST 16  
||| ||| ||| ||| |||  
DB 437 GRFSSPRRRFSGSS 450

```

RESULT 40
O4CHC7
steroid 17alpha-monooxygenase (EC 1.14.99.9) cytochrome P450 17 - chicken
N:Alternate names: cytochrome P450(c17); steroid 17alpha-hydroxylase
C:Species: Gallus gallus (chicken)
C>Date: 30-Jun-1989 #sequence_revision 30-Jun-1989 #text_change 09-Jul-2004
C:Accession: J070318
R:Ono, H.; Iwasaki, M.; Sakamoto, N.; Mizuno, S.
Gene 66, 77-85, 1988
A:Title: cDNA cloning and sequence analysis of a chicken gene expressed during the gonad
A:Reference number: J070318; MUID:88323730; PMID:3047010
A:Accession: J070318
A:Molecule type: mRNA
A:Residues: 1-508 <ONO>
A:Cross-references: UNIPROT:P12394; UNIPARC:UPI0000128307; GR:M21406; NID:g212492; PIDN:
C:Superfamily: human cytochrome P450 CYP2D6; cytochrome P450 homology
C:Keywords: chromoprotein; heme; iron; metalloprotein; monooxygenase; ovary; oxidoreduct
F:302-467/Domain: cytochrome P450 homology <CYP>
F:445/Binding site: heme iron (Cys) (axial ligand) #status predicted

Query Match          44.0%; Score 40; DB 1; Length 508;
Best Local Similarity 60.0%; Pred. No. 86;
Matches 9; Conservative 1; Mismatches 5; Indels 0; Gaps 0;

QY      4 RLSYSRRRSTSTGR 18
Db      18 RLSYSQGPTGTGTR 32

```

Search completed: May 21, 2006, 00:24:47  
 Job time : 40 secs



GenCore version 5.1.8  
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OM protein - protein search, using sw model

Run on: May 21, 2006, 00:15:45 ; Search time 295 Seconds  
(without alignments)  
56.442 Million cell updates/sec

Title: US-09-857-000a-11

Perfect score: 91

Sequence: 1 RGRLSYSRRRSTSTGR 18

Scoring table:

BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 2849598 seqs, 925015592 residues

Total number of hits satisfying chosen parameters: 2849598

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 100 summaries

Database : UniProt\_7.2.\*

1: uniprot\_sprot.\*

2: uniprot\_trembl.\*

Pred. No. is the number of results predicted by chance to have a  
score greater than or equal to the score of the result being printed,  
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	61	67.0	149	1 PG1_PIG	P212194 sus scrofa
2	56	61.5	109	2 Q70V15_9VIRU	Q70V15 daphne viru
3	55	60.4	147	1 PG2_PIG	P32195 sus scrofa
4	54	59.3	149	1 PG3_PIG	P32196 sus scrofa
5	54	59.3	149	1 PG5_PIG	P49934 sus scrofa
6	52	57.1	173	2 Q9ETA8_COREQ	Q9ETA8 corynebacte
7	51	56.0	108	2 Q80P41_9VIRU	Q80P41 narcissus c
8	50	54.9	109	2 Q5GR18_9VIRU	Q5GR18 daphne viru
9	49	53.8	476	1 GATB_LACJO	P61344 lactobacill
10	48	52.7	102	2 Q80P37_9VIRU	Q80P37 narcissus c
11	48	52.7	1062	2 Q4W9D8_ASPTU	Q4W9D8 aspergillus
12	47	51.6	91	2 Q68IP8_9VIRU	Q68IP8 potato viru
13	47	51.6	92	2 Q38024_9VIRU	Q38024 potato viru
14	47	51.6	93	2 Q73508_9VIRU	Q73508 potato viru
15	47	51.6	93	2 Q73509_9VIRU	Q73509 potato viru
16	47	51.6	93	2 Q73512_9VIRU	Q73512 potato viru
17	47	51.6	93	2 Q73514_9VIRU	Q73514 potato viru
18	47	51.6	93	2 Q73527_9VIRU	Q73527 potato viru
19	47	51.6	93	2 Q73529_9VIRU	Q73529 potato viru
20	47	51.6	93	2 Q73531_9VIRU	Q73531 potato viru
21	47	51.6	93	2 Q93139_9VIRU	Q93139 potato viru
22	47	51.6	94	2 Q73525_9VIRU	Q73525 potato viru
23	47	51.6	94	2 Q4A305_9VIRU	Q4A305 potato viru
24	47	51.6	94	2 Q4U6V1_9VIRU	Q4U6V1 potato viru
25	47	51.6	94	2 Q6R5K2_9VIRU	Q6R5K2 potato viru
26	47	51.6	94	2 Q86541_9VIRU	Q86541 potato viru
27	47	51.6	391	2 Q3MVD3_9DELTA	Q3MVD3 syntrophoba
28	46.5	51.1	699	2 Q55Q95_CRYNE	Q55Q95 cryptococcu
29	46.5	51.1	699	2 Q5KFX2_CRYNE	Q5KFX2 cryptococcu
30	46	50.5	94	2 Q41486_9VIRU	Q41486 potato viru
31	46	50.5	233	2 Q3FAL7_9BURK	Q3FAL7 burkholderi

ALIGNMENTS

32	46	50.5	236	2	O16689_CABEL	O16689 caenorhabdi
33	45.5	50.0	288	2	Q7PPP7_MACRU	Q7PPP7 anopheles g
34	45	49.5	59	1	HSP1_MACRU	P42142 macropus ru
35	45	49.5	60	1	HSP1_CAEFU	P42131 caenolestes
36	45	49.5	60	1	HSP1_DASHA	P67834 dasyurus ha
37	45	49.5	60	1	HSP1_DENGO	P67838 dendrolagus
38	45	49.5	60	1	HSP1_MACAG	P42137 macropus ag
39	45	49.5	60	1	HSP1_MACAG	Q9GL9 macropus pa
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41	45	49.5	60	1	HSP1_ONYUN	P67839 onychogalea
42	45	49.5	60	1	HSP1_POTLO	Q9GL98 potorous lo
43	45	49.5	60	1	HSP1_SETR	P67840 setonix bra
44	45	49.5	61	1	HSP1_ANTLA	O18745 antechinomy
45	45	49.5	61	1	HSP1_BETPE	Q9GL90 betongia p
46	45	49.5	61	1	HSP1_DASGE	P67851 dasyurus al
47	45	49.5	61	1	HSP1_DASGE	P67850 dasyurus ge
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50	45	49.5	61	1	HSP1_DASVI	P67835 dasyurus vi
51	45	49.5	61	1	HSP1_LAGFI	Q86696 lagostrophu
52	45	49.5	61	1	HSP1_NBOLO	P67852 neophascoga
53	45	49.5	61	1	HSP1_PABRI	O18758 parantechin
54	45	49.5	61	1	HSP1_PHADO	P67853 phascospor
55	45	49.5	61	1	HSP1_SARHA	P62486 sarcophilus
56	45	49.5	61	1	HSP1_SMILO	Q9TUC2 sminthopsis
57	45	49.5	62	1	HSP1_ANTBE	Q71V18 antechinus
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67	45	49.5	62	1	HSP1_DASBY	Q71V97 dasyuroides
68	45	49.5	62	1	HSP1_DASCR	Q71V98 dasyercus
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72	45	49.5	62	1	HSP1_MYOME	Q71VH0 myoictis me
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75	45	49.5	62	1	HSP1_NINRI	Q71V97 ningau rid
76	45	49.5	62	1	HSP1_NINTI	Q71V95 ningau tim
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79	45	49.5	62	1	HSP1_PACAL	Q71V10 phascogale
80	45	49.5	62	1	HSP1_PHTA	P67847 phascogale
81	45	49.5	62	1	HSP1_PPLAM	Q71V94 planigale m
82	45	49.5	62	1	HSP1_PSEMD	P67832 pseudantech
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85	45	49.5	62	1	HSP1_SMIAT	Q71V99 sminthopsis
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87	45	49.5	62	1	HSP1_SMIAT	Q9TUC4 sminthopsis
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89	45	49.5	62	1	HSP1_SMIAT	Q71V97 sminthopsis
90	45	49.5	62	1	HSP1_SMIAT	Q71V96 sminthopsis
91	45	49.5	62	1	HSP1_SMIAT	Q71V94 sminthopsis
92	45	49.5	62	1	HSP1_SMIAT	Q71V95 sminthopsis
93	45	49.5	62	1	HSP1_SMIAT	Q71V93 sminthopsis
94	45	49.5	62	1	HSP1_SMIAT	Q71V92 sminthopsis
95	45	49.5	62	1	HSP1_SMIAT	Q71V98 sminthopsis
96	45	49.5	62	1	HSP1_SMIAT	Q71V99 sminthopsis
97	45	49.5	62	1	HSP1_SMIAT	Q71V91 sminthopsis
98	45	49.5	62	1	HSP1_SMIAT	Q71V90 sminthopsis
99	45	49.5	62	1	HSP1_SMIAT	Q71V99 sminthopsis
100	45	49.5	62	1	HSP1_SMIAT	Q71V98 sminthopsis

RESULT 1  
PGL\_PIG STANDARD; PRT; 149 AA.  
AC P32194;  
DT 01-OCT-1993, integrated into UniProtKB/Swiss-Prot.  
DT 01-OCT-1996, sequence version 2.  
DT 07-FEB-2006, entry version 49.  
DE Protegrin-1 precursor (PG-1) (Neutrophil peptide 1).  
GN #Name=NGP1;  
OS Sus scrofa (pig).  
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
OC Mammalia; Eutheria; Laurasiatheria; Cetartiodactyla; Suina; Suidae;  
OC Sus.  
OX NCBI\_TaxID=9823;  
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RP NUCLEOTIDE SEQUENCE.  
RC TISSUE=Bone marrow;  
RX MEDLINE=94283613; PubMed=8013647; DOI=10.1016/0014-5793(94)00493-5;  
RA Zhao C., Liu L., Lehrer R.I.;  
RT "Identification of a new member of the protegrin family by cDNA  
cloning.";  
RL FEBS Lett. 346:285-288 (1994).  
RN [2]  
RP NUCLEOTIDE SEQUENCE.  
RC STRAIN=Red Duroc;  
RX MEDLINE=95354835; PubMed=7628604; DOI=10.1016/0014-5793(95)00633-K;  
RA Zhao C., Ganz T., Lehrer R.I.;  
RT "The structure of porcine protegrin genes.";  
RL FEBS Lett. 368:197-202 (1995).  
RN [3]  
RP PROTEIN SEQUENCE OF 131-148.  
RC TISSUE=Leukocyte; PubMed=8335113; DOI=10.1016/0014-5793(93)80175-T;  
RX MEDLINE=93327946; PubMed=8335113; DOI=10.1016/0014-5793(93)80175-T;  
RA Kokryakov V.N., Harwig S.S.L., Fanyutich E.A., Shevchenko A.A.,  
Alleshina G.M., Shamova O.V., Korneva H.A., Lehrer R.I.;  
RT "Protegrins: leukocyte antimicrobial peptides that combine features of  
corticostatic defensins and tachyplesins.";  
RL FEBS Lett. 327:231-236 (1993).  
RN [4]  
RP PROTEIN SEQUENCE OF 131-148.  
RC TISSUE=Neutrophil;  
RX MEDLINE=93387466; PubMed=8375505; DOI=10.1016/0014-5793(93)80900-P;  
RA Margorodskaya O.A., Shevchenko A.A., Abdalla K.O.M.A.,  
Chernushevich I.V., Egorov T.A., Musoliamov A.X., Kokryakov V.N.,  
Shamova O.V.;  
RT "Primary structure of three cationic peptides from porcine  
neutrophils. Sequence determination by the combined usage of  
electrospray ionization mass spectrometry and Edman degradation.";  
RL FEBS Lett. 330:339-342 (1993).  
RN [5]  
RP STRUCTURE BY NMR OF PROTEGRIN 1.  
RX MEDLINE=96235220; PubMed=8647100;  
RA Amelase A., Mangoni M., Roumestand C., Chiche L., Despaux E.,  
Grassy G., Calas B., Chavanieu A.;  
RT "Synthesis and solution structure of the antimicrobial peptide  
protegrin-1.";  
RL Eur. J. Biochem. 237:575-583 (1996).  
RN [6]  
RP STRUCTURE BY NMR OF PROTEGRIN 1.  
RX MEDLINE=97113279; PubMed=8807886; DOI=10.1016/S1074-5521(96)90145-3;  
RA Fahrner R.L., Dieckmann T., Harwig S.S., Lehrer R.I., Eisenberg D.,  
Feigon J.;  
RT "Solution structure of protegrin-1, a broad-spectrum antimicrobial  
peptide from porcine leukocytes.";  
RL Chem. Biol. 3:543-550 (1996).  
CC -1- FUNCTION: Microbicidal activity. Active against E.coli, Listeria  
monocytogenes and C.albicans in vitro.  
CC -1- SUBCELLULAR LOCATION: Secreted protein.  
CC -1- SIMILARITY: Belongs to the cathelicidin family.  
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DR EMBL; X79868; CAA56251.1; -; mRNA.  
DR EMBL; X84094; CAA58890.1; -; Genomic\_DNA.  
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DR Pfam; PF00666; Cathelicidins; 1.  
DR ProDom; PD001838; Cathelicidin; 1.  
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FT similarity).  
FT MOD\_RES 148 148 Arginine amide (G-149 provides amide  
FT group).  
FT DISULFID 85 96 By similarity.  
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FT DISULFID 138 143  
FT STRAND 133 139  
FT TURN 140 141  
FT STRAND 142 147  
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Query Match 67.0%; Score 61; DB 1; Length 149;  
Best Local Similarity 66.7%; Score No. 0.031;  
Matches 12; Conservative 0; Mismatches 6; Indels 0; Gaps 0;  
QY 1 RGGRLSYRRRFRSTGTR 18  
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DB 131 RGGRLCYCRRFCVCVGR 148  
RESULT 2  
Q70VI5\_9VIRU  
ID Q70VI5\_9VIRU PRELIMINARY; PRT; 109 AA.  
AC Q70VI5;  
DT 05-JUL-2004, integrated into UniProtKB/TrEMBL.  
DT 05-JUL-2004, sequence version 1.  
DT 07-FEB-2006, entry version 9.  
DE Hypothetical 12K protein.  
OS Daphne virus S  
OC Viruses; ssRNA positive-strand viruses, no DNA stage; Flexiviridae;  
OC Carlavirus.  
OX NCBI\_TaxID=216614;  
RN [1]  
RP NUCLEOTIDE SEQUENCE.  
RC STRAIN=Kr2;  
RX MEDLINE=22897970; PubMed=14551815; DOI=10.1007/s00705-003-0161-2;  
RA Lee B.Y., Choi S.H., Ryu K.H.;  
RT "Characterization of the 3'-terminal nucleotide sequence of two Korean  
isolates of Daphne virus S support its placement as a distinct species  
of the genus Carlavirus.";  
RL Arch. Virol. 148:1915-1924 (2003).  
RN [2]  
RP NUCLEOTIDE SEQUENCE.  
RC STRAIN=Kr2;  
RA Ryu K.;  
RL Submitted (DEC-2002) to the EMBL/GenBank/DBJ databases.  
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CC  
CC EMBL; AJ535085; CAD59393.1; -; Genomic RNA.  
CC GO; GO:0003676; F:nucleic acid binding; IEA.



DR GO: 0006355; P: regulation of transcription, DNA-dependent; IEA.  
 DR InterPro: IPR002569; Carla\_Bd.  
 DR Pfam: PF01623; Carla\_C4; 1.  
 KW Hypothetical protein.  
 SQ SEQUENCE 109 AA; 12328 MW; BC0338DEB44CED84 CRC64;  
 Query Match 61.5%; Score 56; DB 2; Length 109;  
 Best Local Similarity 64.7%; Pred. No. 0.16;  
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 DT 01-OCT-1996, sequence version 2.  
 DT 07-FEB-2006, entry version 43.  
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 OC Sus.  
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 RN [1]  
 RP NUCLEOTIDE SEQUENCE [MRNA].  
 RC TISSUE=Bone marrow;  
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 RA Storicci P., Zanetti M.;  
 RT "A novel cDNA sequence encoding a pig leukocyte antimicrobial peptide  
 with a cathelin-like pro-sequence.";  
 RT Blochem. Biophys. Res. Commun. 196:1363-1368(1993).  
 RL [2]  
 RP PROTEIN SEQUENCE OF 131-146.  
 RC TISSUE=Leukocyte;  
 RX MEDLINE=93327946; PubMed=8335113; DOI=10.1016/0014-5793(93)80175-T;  
 RA Kokryakov V.N., Harwig S.S.L., Panyutich E.A., Shevchenko A.A.,  
 RA Aleshina G.M., Shamova O.V., Korneva H.A., Lehrer R.I.;  
 RT "Protegrins: leukocyte antimicrobial peptides that combine features of  
 corticostatic defensins and tachyplesins.";  
 RL FEBS Lett. 327:231-236(1993).  
 CC -1- FUNCTION: Microbicidal activity. Active against E.coli, Listeria  
 CC monocytes and C.albicans, in vitro.  
 CC -1- SUBCELLULAR LOCATION: Secreted protein.  
 CC -1- SIMILARITY: Belongs to the cathelicidin family.  
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 DR EMBL; L24745; AAA31061.1; -; mRNA.  
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 DR HSSP; P32196; 1LXE.  
 DR SMR; P32195; 30-130.  
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 DR PANTHER; PTHR10206; Cathelicidins; 1.  
 DR Pfam; PF00666; Cathelicidins; 1.  
 DR ProDom; PD001838; Cathelicidins; 1.  
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 DR PROSITE; PS00947; CATHELICIDINS 2; 1.  
 KW Amidation; Antibiotic; Antimicrobial; Direct protein sequencing;  
 KW Pyrolydione carboxylic acid; Signal.  
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FT MOD\_RES 146 146 Valine amide (G-147 provides amide  
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 FT DISULFID 107 124 By similarity.  
 FT DISULFID 136 145 By similarity.  
 FT DISULFID 138 143 By similarity.  
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 Db 131 RGRLCYCRRRFCICVG 147  
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 AC P32196;  
 DT 01-OCT-1993, integrated into UniProtKB/Swiss-Prot.  
 DT 01-OCT-1996, sequence version 2.  
 DT 07-FEB-2006, entry version 47.  
 DE Protegrin-3 precursor (PG-3).  
 GN Name=PG3;  
 OS Sus scrofa (Pig).  
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
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 OC Sus.  
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 RP NUCLEOTIDE SEQUENCE.  
 RC TISSUE=Bone marrow;  
 RX MEDLINE=94283613; PubMed=8013647; DOI=10.1016/0014-5793(94)00493-5;  
 RA Zhao C., Liu L., Lehrer R.I.;  
 RT "Identification of a new member of the protegrin family by cDNA  
 cloning.";  
 RL FEBS Lett. 346:285-288(1994).  
 RN [2]  
 RP NUCLEOTIDE SEQUENCE.  
 RC STRAIN=Red Duroc;  
 RX MEDLINE=95354835; PubMed=7628604; DOI=10.1016/0014-5793(95)00633-K;  
 RA Zhao C., Ganz T., Lehrer R.I.;  
 RT "The structure of porcine protegrin genes.";  
 RL FEBS Lett. 368:197-202(1995).  
 RN [3]  
 RP PROTEIN SEQUENCE OF 131-148.  
 RC TISSUE=Leukocyte;  
 RX MEDLINE=93327946; PubMed=8335113; DOI=10.1016/0014-5793(93)80175-T;  
 RA Kokryakov V.N., Harwig S.S.L., Panyutich E.A., Shevchenko A.A.,  
 RA Aleshina G.M., Shamova O.V., Korneva H.A., Lehrer R.I.;  
 RT "Protegrins: leukocyte antimicrobial peptides that combine features of  
 corticostatic defensins and tachyplesins.";  
 RL FEBS Lett. 327:231-236(1993).  
 CC -1- FUNCTION: Microbicidal activity. Active against E.coli, Listeria  
 CC monocytes and C.albicans, in vitro.  
 CC -1- SUBCELLULAR LOCATION: Secreted protein.  
 CC -1- SIMILARITY: Belongs to the cathelicidin family.  
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 DR EMBL; X83267; CAA58240.1; -; mRNA.  
 DR EMBL; X84095; CAA58891.1; -; Genomic\_DNA.  
 DR PIR; S66285; A53895.  
 DR PDB; 1KWI; X-ray; A=30-130.  
 DR PDB; 1LXE; X-ray; A=30-130.  
 DR PDB; 1PFP; X-ray; A=30-130.  
 DR InterPro; IPR001894; Cathelicidin.  
 DR PANTHER; PTHR10206; Cathelicidins; 1.  
 DR Pfam; PF00666; Cathelicidins; 1.  
 DR ProDom; PD001838; Cathelicidins; 1.

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FT	STRAND	98	98		
FT	TURN	100	101		
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FT	STRAND	121	126		
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Query Match 59.3%; Score 54; DB 1; Length 149;  
Best Local Similarity 61.1%; Pred. No. 0.52;  
Matches 11; Conservative 0; Mismatches 7; Indels 0; Gaps 0;

Qy 1 RGRLSYRRRFRSTGR 18  
Db 131 RGGGLCYRRRRCVCVGR 148

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RESULT 5
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AC   P49934;
DT   01-OCT-1996, integrated into UniProtKB/Swiss-Prot.
DT   01-OCT-1996, sequence version 1.
DT   07-FEB-2006, entry version 38.
DE   Protegrin-5 precursor (PG-5).
GN   Name=PG5;
GS   Sus scrofa (Pig).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Euthera; Laurasiatheria; Cetartiodactyla; Suina; Suidae;
OC   Sus.
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RP   NUCLEOTIDE SEQUENCE [GENOMIC DNA].
RC   STRAIN=Red Duroc;
RX   MZLN01=55354835; PubMed:7628604; DOI=10.1016/0014-5793(95)00633-K;
RA   Zhao C., Ganz T., Lehrer R.I.;
RT   "The structure of porcine protegrin genes.";
RL   FEBS Lett. 368.197-202(1995).
CC   -1- FUNCTION: Microbicidal activity (By similarity).
CC   -1- SUBCELLULAR LOCATION: Secreted protein.
CC   -1- SIMILARITY: Belongs to the cathelicidin family.
CC   Copyrighted by the UniProt Consortium, see http://www.uniprot.org/
CC   Distributed under the Creative Commons Attribution-NoDerivs License
CC   EMBL: X84096; CAA58892.1; -; Genomic_DNA.
DR   PIR: S66283; S57609.
DR   HSPB: P32196; IUXE.
DR   SWR: P49934; 30-130.
DR   InterPro: IPR001894; Cathelicidin.
DR   PANTHER: PTHR10206; Cathelicidin; 1.
DR   Pfam: PF00666; Cathelicidins; 1.

```

DR	ProDom; PD001838; Cathelicidin; 1.	1	29	Potential.
DR	PROSTRE; PS00946; CATHELICIDINS_1; 1.	30	130	Potential.
DR	PROSTRE; PS00947; CATHELICIDINS_2; 1.			/FTId=PRO_00000004752.
KW	Amidation; Antibiotic; Antimicrobial; Pyrrolidone carboxylic acid;	131	148	Protegrin-5.
KW	Signal.			/FTId=PRO_00000004753.
FT	SIGNAL	30	30	Pyrrolidone carboxylic acid (By
FT	PROPEP			similarity).
FT	PEPTIDE	148	148	Arginine amide (G-149 provides amide
FT	MOD_RES			group) (By similarity).
FT	MOD_RES	85	96	By similarity.
FT	DISULFID	107	124	By similarity.
FT	DISULFID	136	145	By similarity.
FT	DISULFID	138	143	By similarity.
FT	SEQUENCE	149 AA;	156	By similarity.
SO	SEQUENCE	149 AA;	15604 MW;	6CC7262429CD6B64 CRC64;

Query Match	59.3%	Score 54;	DB 1;	Length 149;
Best Local Similarity	61.1%	Pred. No. 0.52;		
Matches 11;	Conservative	0;	Mismatches 7;	Indels 0;
			Gaps	0;

Qy 1 RGGRLSYSRRRFSTSTGR 18  
|||  
Db 131 RGGRLCYCRPRFCTCVGR 148  
|||

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RESULT 6
ID Q9ETA8 COREQ Q9ETA8 COREQ PRELIMINARY; PRT; 173 AA.
AC Q9ETA6;
DT 01-MAR-2001, integrated into UniProtKB/TrEMBL.
DT 01-MAR-2001, sequence version 1.
DT 07-FEB-2006, entry version 15.
DE Hypothetical protein orf58.
GN Name=orf58;
OS Corynebacterium equi (Rhodococcus equi).
OG Plasmid pREAT701 (p33701), and plasmid virulence plasmid.
OC Bacteria; Actinobacteria; Actinobacteridae; Actinomycetales;
OC Corynebacterineae; Nocardiaceae; Rhodococcus.
OX NCBI_TaxID=433767;
[1]
RN NUCLEOTIDE SEQUENCE.
RC STRAIN=103, and ATCC33701; PLASMID=pREAT701 (p33701), and virulence
RC plasmid;
RX MEDLINE=20536428; PubMed=11083803;
RX DOI=10.1128/IAI.68.12.6840-6847.2000;
RA Takai S., Hines S.A., Sekizaki T., Nicholson V.M., Alperin D.A.,
RA Osaki M., Takamatsu D., Nakamura M., Suzuki K., Ogino N., Kakuda T.,
RA Dan H., Prescott J.P.;
RT "DNA sequence and comparison of virulence plasmids from Rhodococcus
RT equi ATCC 33701 and 103.";
RL Infect. Immun. 68:6840-6847(2000).
-----
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-----
EMBL; AP001204; BAB16667.1; -; Genomic DNA.
DR EMBL; AF116907; AAG21761.1; -; Genomic DNA.
DR Hypothetical protein; Plasmid.
SQ SEQUENCE 173 AA; 18852 MW; F18A637BCAA04053 CRC64;

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Query Match	57.1%	Score 52;	DB 2;	Length 173;
Best Local Similarity	52.9%	Pred. No. 1.4;		
Matches	9;	Conservative	4;	Mismatches 4;
			Indels	0;
			Gaps	0;

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QY      2  GGRLSYSRRRFSTSTGR 18
      |||:|:|:|:|
Db     142 GGRISYASLRYTDETGR 158
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SQ SEQUENCE 109 AA; 12364 MW; 2AB2455E9FB8E510 CRC64;  
 Query Match 54.9%; Score 50; DB 2; Length 109;  
 Best Local Similarity 58.8%; Pred. No. 1.8;  
 Matches 10; Conservative 3; Mismatches 4; Indels 0; Gaps 0;  
 QY 2 GGRLSYRRRFFSTGTGR 18  
 |||||:|:|:|  
 DB 42 GGRSSYARKRRALSIGR 58  
 |||||:|:|:|

RESULT 9  
 GATB\_LACJO STANDARD; PRT; 476 AA.  
 ID GATB\_LACJO  
 AC P61344;  
 DT 10-MAY-2004, integrated into UniProtKB/Swiss-Prot.  
 DT 10-MAY-2004, sequence version 1.  
 DT 07-MAR-2006, entry version 14.  
 DE Aspartyl/glutamyl-tRNA (Asn/Gln) amidotransferase subunit B  
 DE (EC 6.3.5.-) (Asp/Glu-ADT subunit B).  
 GN Name=gatB; OrderedLocusNames=LJ1716;  
 OS Lactobacillus johnsonii  
 OC Bacteria; Firmicutes; Lactobacillales; Lactobacillaceae;  
 OC Lactobacillus.  
 OC NCBI\_TaxID=33959;  
 RX [1]  
 RP NUCLEOTIDE SEQUENCE [LARGE SCALE GENOMIC DNA].  
 RC PubMed=533;  
 RC PubMed=14983040; DOI=10.1073/pnas.0307327101;  
 RA Fridmore R.D., Berger B., Desiere F., Vilanova D., Barretto C.,  
 RA Pittet A.-C., Zwielen A.-C., Rouvet M., Altermann E., Barrangou R.,  
 RA Mollet B., Mercenier A., Klaenhammer T., Arigoni F., Schell M.A.;  
 RA "The genome sequence of the probiotic intestinal bacterium  
 RT Lactobacillus johnsonii NCC 533.";  
 RL Proc. Natl. Acad. Sci. U.S.A. 101:2512-2517(2004).  
 CC -!- FUNCTION: Allows the formation of correctly charged Asn-tRNA (Asn  
 CC or Gln-tRNA (Gln) through the transamidation of misacylated Asp-  
 CC tRNA (Asn) or Glu-tRNA (Gln) in organisms which lack either or both  
 CC of asparaginyl-tRNA or glutamyl-tRNA synthetases. The reaction  
 CC takes place in the presence of glutamine and ATP through an  
 CC activated phospho-Asp-tRNA (Asn) or phospho-Glu-tRNA (Gln) (By  
 CC similarity).  
 CC -!- CATALYTIC ACTIVITY: ATP + L-glutamyl-tRNA (Gln) + L-glutamine = ADP  
 CC + phosphate + L-glutamyl-tRNA (Gln) + L-glutamate.  
 CC -!- CATALYTIC ACTIVITY: ATP + L-aspartyl-tRNA (Asn) + L-glutamine = ADP  
 CC + phosphate + L-asparaginyl-tRNA (Asn) + L-glutamate.  
 CC -!- SUBUNIT: Heterotrimer of A, B and C subunits (by similarity).  
 CC -!- SIMILARITY: Belongs to the gatB/gatE family. GatB subfamily.  
 CC  
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 CC -----  
 CC EMBL; AB017198; AAC09487.1; -; Genomic\_DNA.  
 CC GenomeReviews; AB017198 GR; LJ1716.  
 CC BioCyc; LJOH257314:LJ1716-MONOMER; -.  
 CC HAMAP; MF 00121; -; 1.  
 CC InterPro; IPR004413; GatB.  
 CC InterPro; IPR006107; GatB\_central.  
 CC InterPro; IPR006075; GatB\_N.  
 CC InterPro; IPR003789; GatB\_Yqey.  
 CC PANTHER; PTHR11659; GatB; 1.  
 CC Pfam; PF01162; GatB; 1.  
 CC Pfam; PF02934; GatB\_N; 1.  
 CC Pfam; PF04637; GatB\_Yqey; 1.  
 CC TIGRFAMs; TIGR00133; gatB; 1.  
 CC PROSITE; PS01234; GATB; 1.  
 CC Complete proteome; Ligase; Protein biosynthesis.  
 CC CHAIN 1 476  
 CC Aspartyl/glutamyl-tRNA (Asn/Gln)  
 CC amidotransferase subunit B.  
 CC /FTID=PROT0000148796.  
 CC

SQ SEQUENCE 476 AA; 53904 MW; 5A13505687A9A014 CRC64;  
 Query Match 53.8%; Score 49; DB 1; Length 476;  
 FT

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Best Local Similarity 52.9%; Pred. No. 15;
Matches 9; Conservative 3; Mismatches 5; Indels 0; Gaps 0;

QY 2 GGRLSYRRRRFSTGTGR 18
Db 239 GGRVQLSTRFDEATGK 255
|||:|||||:|:|:
|||:|||||:|:|:

RESULT 10
Q80P37_9VIRU PRELIMINARY; PRT; 102 AA.
AC Q80P37;
DT 01-JUN-2003, integrated into UniProtKB/TrEMBL.
DT 01-JUN-2003, sequence version 1.
DT 07-FEB-2006, entry version 8.
DE Nucleic acid binding protein.
OS Narcissus common latent virus.
OC Viruses; ssRNA positive-strand viruses, no DNA stage; Flexiviridae;
OC Carlavirus.
OX NCBI_TaxID=160844;
[1]
RN NUCLEOTIDE SEQUENCE.
RP Chen J., Chen J., Langeveld S.A., Derks A.F.L.M., Adams M.J.;
RA "Molecular characterization of carla- and potyvirus from Narcissus
RT in China.";
RL J. Phytopathol. 151:26-29(2003).
CC -----
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CC -----
DR EMBL; AJ311376; CAC85389.1; -; Genomic RNA.
DR GO; GO:0003676; P:nucleic acid binding; IEA.
DR GO; GO:0006355; P:regulation of transcription, DNA-dependent; IEA.
DR InterPro; IPR002568; Carla_bd.
DR Pfam; PF01623; Carla_C4; 1.
SQ SEQUENCE 102 AA; 11446 MW; 929E1615860484CC CRC64;

Query Match 52.7%; Score 48; DB 2; Length 102;
Best Local Similarity 52.9%; Pred. No. 3.7;
Matches 9; Conservative 4; Mismatches 4; Indels 0; Gaps 0;

QY 2 GGRLSYRRRRFSTGTGR 18
Db 40 GGRKSARRRRRAANIGR 56
|||:|||||:|:|:
|||:|||||:|:|:

RESULT 11
Q4W9D8_ASPFU PRELIMINARY; PRT; 1062 AA.
AC Q4W9D8;
DT 05-JUL-2005, integrated into UniProtKB/TrEMBL.
DT 05-JUL-2005, sequence version 1.
DT 07-MAR-2006, entry version 6.
DE Von Willebrand domain protein.
GN CRPFNames-Afu4901160;
OS Aspergillus fumigatus (Sartorya fumigatus).
OC Eukaryota; Fungi; Ascomycota; Pezizomycotina; Eurotiomycetes;
OC Eurotiales; Trichocomaceae; mitosporic Trichocomaceae; Aspergillus.
OX NCBI_TaxID=5085;
[1]
RN NUCLEOTIDE SEQUENCE [LARGE SCALE GENOMIC DNA].
RC STRAIN=Af293 / CBS 101355 / FGSC A1100;
RX PubMed=16372009; DOI=10.1038/nature04332;
RA Nierman W.C., Pain A., Anderson M.J., Wortman J.R., Kim H.S.,
RA Arroyo J., Berriman M., Abe K., Archer D.B., Bermejo C., Bennett J.W.,
RA Bowyer P., Chen D., Collins M., Coulson R., Davies R., Dyer P.S.,
RA Farman N., Fedorova N., Fedorova N.D., Feldblyum T.V., Fischer R.,
RA Foster N., Fraser A., Garcia J.L., Garcia M.J., Goble A.,
RA Goldman G.H., Gomi K., Griffith-Jones S., Gwilliam R., Haas B.J.,
RA Haas H., Harris D.B., Horiuchi H., Huang J., Humphray S., Jimenez J.,
RA Keller N., Khouri H., Kitamoto K., Kobayashi T., Konzack S.,
RA Kulkarni R., Kumagai T., Lafont A., Latge J.-P., Li W., Lord A.,
RA Lu C., Majoros W.H., May G.S., Miller B.L., Mohamoud Y., Molina M.,
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RA Monod M., Mouyna I., Mulligan S., Murphy L.D., O'Neil S., Paulsen I.,
RA Penalba M.A., Perteu M., Price C., Pritchard B.L., Quail M.A.,
RA Rabinowitsch E., Rawlins N., Rajandream M.A., Reichard U.,
RA Renaud H., Robson G.D., Rodriguez de Cordoba S., Rodriguez-Pena J.M.,
RA Roming C.M., Rutter S., Salzberg S.L., Sanchez M.,
RA Sanchez-Ferrero J.C., Saunders D., Seeger K., Squares R., Squares S.,
RA Takeuchi M., Tekalia F., Turner G., Vazquez de Aldana C.R., Weidman J.,
RA White O., Woodward J.R., Yu J.-H., Fraser C.M., Galagan J.E., Asai K.,
RA Machida M., Hall N., Barrell B.G., Denning D.W.;
RT "Genomic sequence of the pathogenic and allergenic filamentous fungus
RT Aspergillus fumigatus.";
RL Nature 438:1151-1156(2005).
CC -!- CAUTION: The sequence shown here is derived from an
CC EMBL/GenBank/DBJ whole genome shotgun (WGS) entry which is
CC preliminary data.
CC -----
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CC -----
DR EMBL; AAHP01000017; EAL84303.1; -; Genomic_DNA.
DR InterPro; IPR006587; VIT.
DR InterPro; IPR002035; VWF_A.
DR Pfam; PF00092; VWA; 1.
DR SMART; SM00327; VWA; 1.
DR PROSITE; PS50234; VWEA; 1.
DR Complete proteome.
KW Complete proteome.
SQ SEQUENCE 1062 AA; 117219 MW; EF2F3AF2B1B5F84B CRC64;

Query Match 52.7%; Score 48; DB 2; Length 1062;
Best Local Similarity 61.1%; Pred. No. 55;
Matches 11; Conservative 0; Mismatches 7; Indels 0; Gaps 0;

QY 1 RGRLSYRRRRFSTGTGR 18
Db 719 RGCLLSYPRREFLASTSR 736
|||:|||||:|:|:
|||:|||||:|:|:

RESULT 12
Q68IP8_9VIRU PRELIMINARY; PRT; 91 AA.
AC Q68IP8;
DT 11-OCT-2004, integrated into UniProtKB/TrEMBL.
DT 11-OCT-2004, sequence version 1.
DT 11-FEB-2006, entry version 7.
DE 11k protein.
OS Potato virus S.
OC Viruses; ssRNA positive-strand viruses, no DNA stage; Flexiviridae;
OC Carlavirus.
OX NCBI_TaxID=12169;
[1]
RN NUCLEOTIDE SEQUENCE.
RP Lang Q., Chen J., Du Z.;
RA "Molecular Identification of PVS in Hangzhou.";
RT Submitted (JUL-2004) to the EMBL/GenBank/DBJ databases.
CC -----
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CC -----
DR EMBL; AY687337; AAT97709.1; -; Genomic RNA.
DR GO; GO:0003676; P:nucleic acid binding; IEA.
DR GO; GO:0006355; P:regulation of transcription, DNA-dependent; IEA.
DR InterPro; IPR002568; Carla_bd.
DR Pfam; PF01623; Carla_C4; 1.
SQ SEQUENCE 91 AA; 10264 MW; 02A0F98659B9812D CRC64;

Query Match 51.6%; Score 47; DB 2; Length 91;
Best Local Similarity 52.9%; Pred. No. 4.8;
Matches 9; Conservative 4; Mismatches 4; Indels 0; Gaps 0;

QY 2 GGRLSYRRRRFSTGTGR 18
Db 38 GGRSTYARRRRRSIGR 54
|||:|||||:|:|:
|||:|||||:|:|:
```

```
RESULT 13
O38024 9VIRU PRELIMINARY; PRT; 92 AA.
ID O38024
AC O38024
DT 01-JAN-1998, integrated into UniProtKB/TrEMBL.
DT 01-JAN-1998, sequence version 1.
DT 07-FEB-2006, entry version 22.
DE Hypothetical protein.
OS Potato virus M.
OC Viruses; ssRNA positive-strand viruses, no DNA stage; Flexiviridae;
OC Carlavirus.
OX NCBI_TaxID=12167;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RC STRAIN=Idaho;
RA Caviller T.D.; Corsini D.L.; Berger P.H.;
RL Submitted (SEP-1997) to the EMBL/GenBank/DBJ databases.
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CC -----
EMBL; AF023877; AAB81273.1; -; Genomic RNA.
DR GO; GO:0003676; P:nucleic acid binding; IEA.
DR GO; GO:0006355; P:regulation of transcription, DNA-dependent; IEA.
DR InterPro; IPR002568; Carla_bd.
DR Pfam; PF01623; Carla_C4; 1.
DR Hypothetical protein.
KW Hypothetical protein.
SQ SEQUENCE 92 AA; 10319 MW; B0A9ACT0B579A980 CRC64;

Query Match 51.6%; Score 47; DB 2; Length 92;
Best Local Similarity 52.9%; Pred. No. 4.9;
Matches 9; Conservative 3; Mismatches 5; Indels 0; Gaps 0;

QY 2 GGRLSYRRRFFSTGTGR 18
||| :||| :|||
DB 40 GGRSKYARRRAAAGR 56

RESULT 14
O73508 9VIRU PRELIMINARY; PRT; 93 AA.
ID O73508
AC O73508
DT 01-AUG-1998, integrated into UniProtKB/TrEMBL.
DT 01-AUG-1998, sequence version 1.
DT 07-FEB-2006, entry version 18.
DE 11K protein (Fragment).
OS Potato virus S.
OC Viruses; ssRNA positive-strand viruses, no DNA stage; Flexiviridae;
OC Carlavirus.
OX NCBI_TaxID=12169;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RC STRAIN=Aschersleben;
RA Matousek J.; Schubert J.; Dedic P.; Ptacek J.;
RT "A broad variability of potato virus S (PVS) revealed by analysis of
RT virus sequences amplified by reverse transcriptase-polymerase chain
RT reaction.";
RL Can. J. Plant Pathol. 22:22-29(2000).
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CC -----
EMBL; Y15613; CAA75702.1; -; Genomic DNA.
DR GO; GO:0003676; P:nucleic acid binding; IEA.
DR GO; GO:0006355; P:regulation of transcription, DNA-dependent; IEA.
DR InterPro; IPR002568; Carla_bd.
DR Pfam; PF01623; Carla_C4; 1.
DR NON_TER 93
SQ SEQUENCE 93 AA; 10521 MW; 2DA6E2925A8C475D CRC64;

Query Match 51.6%; Score 47; DB 2; Length 93;
Best Local Similarity 52.9%; Pred. No. 5;
Matches 9; Conservative 4; Mismatches 4; Indels 0; Gaps 0;

QY 2 GGRLSYRRRFFSTGTGR 18
||| :||| :|||
DB 38 GGRSTYARKRRARSIGR 54

RESULT 15
O73509 9VIRU PRELIMINARY; PRT; 93 AA.
ID O73509
AC O73509
DT 01-AUG-1998, integrated into UniProtKB/TrEMBL.
DT 01-AUG-1998, sequence version 1.
DT 07-FEB-2006, entry version 18.
DE 11K protein (Fragment).
OS Potato virus S.
OC Viruses; ssRNA positive-strand viruses, no DNA stage; Flexiviridae;
OC Carlavirus.
OX NCBI_TaxID=12169;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RC STRAIN=Aschersleben;
RA Matousek J.; Schubert J.; Dedic P.; Ptacek J.;
RT "A broad variability of potato virus S (PVS) revealed by analysis of
RT virus sequences amplified by reverse transcriptase-polymerase chain
RT reaction.";
RL Can. J. Plant Pathol. 22:22-29(2000).
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CC -----
EMBL; Y15615; CAA75706.1; -; Genomic DNA.
DR GO; GO:0003676; P:nucleic acid binding; IEA.
DR GO; GO:0006355; P:regulation of transcription, DNA-dependent; IEA.
DR InterPro; IPR002568; Carla_bd.
DR Pfam; PF01623; Carla_C4; 1.
DR NON_TER 93
SQ SEQUENCE 93 AA; 10521 MW; 2DA6E2925A8C475D CRC64;

Query Match 51.6%; Score 47; DB 2; Length 93;
Best Local Similarity 52.9%; Pred. No. 5;
Matches 9; Conservative 4; Mismatches 4; Indels 0; Gaps 0;

QY 2 GGRLSYRRRFFSTGTGR 18
||| :||| :|||
DB 38 GGRSTYARKRRARSIGR 54

RESULT 16
O73512 9VIRU PRELIMINARY; PRT; 93 AA.
ID O73512
AC O73512
DT 01-AUG-1998, integrated into UniProtKB/TrEMBL.
DT 01-AUG-1998, sequence version 1.
DT 07-FEB-2006, entry version 18.
DE 11K protein (Fragment).
OS Potato virus S.
OC Viruses; ssRNA positive-strand viruses, no DNA stage; Flexiviridae;
OC Carlavirus.
OX NCBI_TaxID=12169;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RC STRAIN=Karla;
RA Matousek J.; Schubert J.; Dedic P.; Ptacek J.;
RT "A broad variability of potato virus S (PVS) revealed by analysis of
RT virus sequences amplified by reverse transcriptase-polymerase chain
RT reaction.";
RL Can. J. Plant Pathol. 22:22-29(2000).
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CC -----
EMBL; Y15611; CAA75698.1; -; Genomic DNA.
DR
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```
Matches 9; Conservative 4; Mismatches 4; Indels 0; Gaps 0;

QY 2 GGRLSYRRRFFSTGTGR 18
||| :||| :|||
DB 38 GGRSTYARKRRARSIGR 54

RESULT 15
O73509 9VIRU PRELIMINARY; PRT; 93 AA.
ID O73509
AC O73509
DT 01-AUG-1998, integrated into UniProtKB/TrEMBL.
DT 01-AUG-1998, sequence version 1.
DT 07-FEB-2006, entry version 18.
DE 11K protein (Fragment).
OS Potato virus S.
OC Viruses; ssRNA positive-strand viruses, no DNA stage; Flexiviridae;
OC Carlavirus.
OX NCBI_TaxID=12169;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RC STRAIN=Aschersleben;
RA Matousek J.; Schubert J.; Dedic P.; Ptacek J.;
RT "A broad variability of potato virus S (PVS) revealed by analysis of
RT virus sequences amplified by reverse transcriptase-polymerase chain
RT reaction.";
RL Can. J. Plant Pathol. 22:22-29(2000).
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CC -----
EMBL; Y15615; CAA75706.1; -; Genomic DNA.
DR GO; GO:0003676; P:nucleic acid binding; IEA.
DR GO; GO:0006355; P:regulation of transcription, DNA-dependent; IEA.
DR InterPro; IPR002568; Carla_bd.
DR Pfam; PF01623; Carla_C4; 1.
DR NON_TER 93
SQ SEQUENCE 93 AA; 10521 MW; 2DA6E2925A8C475D CRC64;

Query Match 51.6%; Score 47; DB 2; Length 93;
Best Local Similarity 52.9%; Pred. No. 5;
Matches 9; Conservative 4; Mismatches 4; Indels 0; Gaps 0;

QY 2 GGRLSYRRRFFSTGTGR 18
||| :||| :|||
DB 38 GGRSTYARKRRARSIGR 54

RESULT 16
O73512 9VIRU PRELIMINARY; PRT; 93 AA.
ID O73512
AC O73512
DT 01-AUG-1998, integrated into UniProtKB/TrEMBL.
DT 01-AUG-1998, sequence version 1.
DT 07-FEB-2006, entry version 18.
DE 11K protein (Fragment).
OS Potato virus S.
OC Viruses; ssRNA positive-strand viruses, no DNA stage; Flexiviridae;
OC Carlavirus.
OX NCBI_TaxID=12169;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RC STRAIN=Karla;
RA Matousek J.; Schubert J.; Dedic P.; Ptacek J.;
RT "A broad variability of potato virus S (PVS) revealed by analysis of
RT virus sequences amplified by reverse transcriptase-polymerase chain
RT reaction.";
RL Can. J. Plant Pathol. 22:22-29(2000).
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CC -----
EMBL; Y15611; CAA75698.1; -; Genomic DNA.
DR
```

```
DR GO:0003676; F:nucleic acid binding; IEA.
DR GO:0006355; P:regulation of transcription, DNA-dependent; IEA.
DR InterPro: IPR002568; Carla_bd.
DR Pfam: PF01623; Carla_C4; 1.
FT NON TER 93
SQ SEQUENCE 93 AA; 10538 MW; 11BD9C9C997BB85 CRC64;

Query Match 51.6%; Score 47; DB 2; Length 93;
Best Local Similarity 52.9%; Pred. No. 5;
Matches 9; Conservative 4; Mismatches 4; Indels 0; Gaps 0;

QY 2 GGRLSYRRRFRSTSTGR 18
DB 38 GGRSTYARRRARSIGR 54

RESULT 17
O73514_9VIRU
ID O73514_9VIRU PRELIMINARY; PRT; 93 AA.
AC O73514;
DT 01-AUG-1998, integrated into UniProtKB/TrEMBL.
DT 01-AUG-1998, sequence version 1.
DT 07-FEB-2006, entry version 18.
DE 11K protein (Fragment).
OS Potato virus S.
OC Viruses; ssRNA positive-strand viruses, no DNA stage; Flexiviridae;
OC Carlavirus.
OX NCBI_TaxID=12169;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RC STRAIN=Karla;
RA Matousek J., Schubert J., Dedic P., Ptacek J.;
RT "A broad variability of pot ato virus S (PVS) revealed by analysis of
RT virus sequences amplified by reverse t ranscriptase-polymerase chain
RT reaction.";
RL Can. J. Plant Pathol. 22:22-29(2000).
CC -----
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CC -----
DR EMBL: Y15612; CAA75700.1; -; Genomic DNA.
DR GO:0003676; F:nucleic acid binding; IEA.
DR GO:0006355; P:regulation of transcription, DNA-dependent; IEA.
DR InterPro: IPR002568; Carla_bd.
DR Pfam: PF01623; Carla_C4; 1.
FT NON TER 93
SQ SEQUENCE 93 AA; 10538 MW; 11BD9C9C997BB85 CRC64;

Query Match 51.6%; Score 47; DB 2; Length 93;
Best Local Similarity 52.9%; Pred. No. 5;
Matches 9; Conservative 4; Mismatches 4; Indels 0; Gaps 0;

QY 2 GGRLSYRRRFRSTSTGR 18
DB 38 GGRSTYARRRARSIGR 54

RESULT 18
O73527_9VIRU
ID O73527_9VIRU PRELIMINARY; PRT; 93 AA.
AC O73527;
DT 01-AUG-1998, integrated into UniProtKB/TrEMBL.
DT 01-AUG-1998, sequence version 1.
DT 07-FEB-2006, entry version 18.
DE 11K protein (Fragment).
OS Potato virus S.
OC Viruses; ssRNA positive-strand viruses, no DNA stage; Flexiviridae;
OC Carlavirus.
OX NCBI_TaxID=12169;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RC STRAIN=Vitava;
RA Matousek J., Schubert J., Dedic P., Ptacek J.;
RT "A broad variability of pot ato virus S (PVS) revealed by analysis of
RT virus sequences amplified by reverse t ranscriptase-polymerase chain
RT reaction.";
RL Can. J. Plant Pathol. 22:22-29(2000).
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CC -----
DR EMBL: Y15612; CAA75700.1; -; Genomic DNA.
DR GO:0003676; F:nucleic acid binding; IEA.
DR GO:0006355; P:regulation of transcription, DNA-dependent; IEA.
DR InterPro: IPR002568; Carla_bd.
DR Pfam: PF01623; Carla_C4; 1.
FT NON TER 93
SQ SEQUENCE 93 AA; 10538 MW; 11BD9C9C997BB85 CRC64;

Query Match 51.6%; Score 47; DB 2; Length 93;
Best Local Similarity 52.9%; Pred. No. 5;
Matches 9; Conservative 4; Mismatches 4; Indels 0; Gaps 0;

QY 2 GGRLSYRRRFRSTSTGR 18
DB 38 GGRSTYARRRARSIGR 54

RESULT 19
O73529_9VIRU
ID O73529_9VIRU PRELIMINARY; PRT; 93 AA.
AC O73529;
DT 01-AUG-1998, integrated into UniProtKB/TrEMBL.
DT 01-AUG-1998, sequence version 1.
DT 07-FEB-2006, entry version 18.
DE 11K protein (Fragment).
OS Potato virus S.
OC Viruses; ssRNA positive-strand viruses, no DNA stage; Flexiviridae;
OC Carlavirus.
OX NCBI_TaxID=12169;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RC STRAIN=Vitava;
RA Matousek J., Schubert J., Dedic P., Ptacek J.;
RT "A broad variability of pot ato virus S (PVS) revealed by analysis of
RT virus sequences amplified by reverse t ranscriptase-polymerase chain
RT reaction.";
RL Can. J. Plant Pathol. 22:22-29(2000).
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CC -----
DR EMBL: Y15616; CAA75708.1; -; Genomic DNA.
DR GO:0003676; F:nucleic acid binding; IEA.
DR GO:0006355; P:regulation of transcription, DNA-dependent; IEA.
DR InterPro: IPR002568; Carla_bd.
DR Pfam: PF01623; Carla_C4; 1.
FT NON TER 93
SQ SEQUENCE 93 AA; 10507 MW; AC2FE2A0F98645C9 CRC64;

Query Match 51.6%; Score 47; DB 2; Length 93;
Best Local Similarity 52.9%; Pred. No. 5;
Matches 9; Conservative 4; Mismatches 4; Indels 0; Gaps 0;

QY 2 GGRLSYRRRFRSTSTGR 18
DB 38 GGRSTYARRRARSIGR 54

RESULT 20
O73531_9VIRU
ID O73531_9VIRU PRELIMINARY; PRT; 93 AA.
AC O73531;
DT 01-AUG-1998, integrated into UniProtKB/TrEMBL.
DT 01-AUG-1998, sequence version 1.
DT 07-FEB-2006, entry version 18.
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RT "A broad variability of pot ato virus S (PVS) revealed by analysis of
RT virus sequences amplified by reverse t ranscriptase-polymerase chain
RT reaction.";
RL Can. J. Plant Pathol. 22:22-29(2000).
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CC -----
DR EMBL: Y15609; CAA75694.1; -; Genomic DNA.
DR GO:0003676; F:nucleic acid binding; IEA.
DR GO:0006355; P:regulation of transcription, DNA-dependent; IEA.
DR InterPro: IPR002568; Carla_bd.
DR Pfam: PF01623; Carla_C4; 1.
FT NON TER 93
SQ SEQUENCE 93 AA; 10333 MW; AB44F80C8018ASC9 CRC64;

Query Match 51.6%; Score 47; DB 2; Length 93;
Best Local Similarity 52.9%; Pred. No. 5;
Matches 9; Conservative 4; Mismatches 4; Indels 0; Gaps 0;

QY 2 GGRLSYRRRFRSTSTGR 18
DB 38 GGRSTYARRRARSIGR 54

RESULT 19
O73529_9VIRU
ID O73529_9VIRU PRELIMINARY; PRT; 93 AA.
AC O73529;
DT 01-AUG-1998, integrated into UniProtKB/TrEMBL.
DT 01-AUG-1998, sequence version 1.
DT 07-FEB-2006, entry version 18.
DE 11K protein (Fragment).
OS Potato virus S.
OC Viruses; ssRNA positive-strand viruses, no DNA stage; Flexiviridae;
OC Carlavirus.
OX NCBI_TaxID=12169;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RC STRAIN=Vitava;
RA Matousek J., Schubert J., Dedic P., Ptacek J.;
RT "A broad variability of pot ato virus S (PVS) revealed by analysis of
RT virus sequences amplified by reverse t ranscriptase-polymerase chain
RT reaction.";
RL Can. J. Plant Pathol. 22:22-29(2000).
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CC -----
DR EMBL: Y15616; CAA75708.1; -; Genomic DNA.
DR GO:0003676; F:nucleic acid binding; IEA.
DR GO:0006355; P:regulation of transcription, DNA-dependent; IEA.
DR InterPro: IPR002568; Carla_bd.
DR Pfam: PF01623; Carla_C4; 1.
FT NON TER 93
SQ SEQUENCE 93 AA; 10507 MW; AC2FE2A0F98645C9 CRC64;

Query Match 51.6%; Score 47; DB 2; Length 93;
Best Local Similarity 52.9%; Pred. No. 5;
Matches 9; Conservative 4; Mismatches 4; Indels 0; Gaps 0;

QY 2 GGRLSYRRRFRSTSTGR 18
DB 38 GGRSTYARRRARSIGR 54

RESULT 20
O73531_9VIRU
ID O73531_9VIRU PRELIMINARY; PRT; 93 AA.
AC O73531;
DT 01-AUG-1998, integrated into UniProtKB/TrEMBL.
DT 01-AUG-1998, sequence version 1.
DT 07-FEB-2006, entry version 18.
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DE 11k protein (Fragment).
OS Potato virus S.
OC Viruses; ssRNA positive-strand viruses, no DNA stage; Flexiviridae;
OC Carlavirus.
OX NCBI_TaxID=12169;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RC STRAIN=Vitava;
RA Matousek J., Schubert J., Dedic P., Ptacek J.;
RT "A broad variability of pot ato virus S (PVS) revealed by analysis of
RT virus sequences amplified by reverse t transcriptase-polymerase chain
RT reaction.";
RL Can. J. Plant Pathol. 22:22-29(2000).
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CC -----
DR EMBL; Y15610; CAA75696.1; -; Genomic DNA.
DR GO; GO:0003676; P:nucleic acid binding; IEA.
DR GO; GO:0006355; P:regulation of transcription, DNA-dependent; IEA.
DR InterPro; IPR002568; Carla_bd.
DR Pfam; PF01623; Carla_C4; 1.
DR NON TER .93
SQ SEQUENCE 93 AA; 10333 MW; AB44F80C8018A5C9 CRC64;

Query Match 51.6%; Score 47; DB 2; Length 93;
Best Local Similarity 52.9%; Pred. No. 5;
Matches 9; Conservative 4; Mismatches 4; Indels 0; Gaps 0;

QY 2 GGRLSYRRRPFSTGCR 18
|||:|:|:|:|
DB 38 GGRSTYARKRRARSIGR 54

RESULT 21
O93139_9VIRU
ID O93139_9VIRU PRELIMINARY; PRT; 93 AA.
AC O93139;
DT 01-NOV-1998, integrated into UniProtKB/TrEMBL.
DT 01-NOV-1998, sequence version 1.
DT 07-FEB-2006, entry version 17.
DE 11k protein (Fragment).
OS Potato virus S.
OC Viruses; ssRNA positive-strand viruses, no DNA stage; Flexiviridae;
OC Carlavirus.
OX NCBI_TaxID=12169;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RC STRAIN=Kobra;
RA Matousek J., Schubert J., Dedic P., Ptacek J.;
RT "A broad variability of pot ato virus S (PVS) revealed by analysis of
RT virus sequences amplified by reverse t transcriptase-polymerase chain
RT reaction.";
RL Can. J. Plant Pathol. 22:22-29(2000).
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CC -----
DR EMBL; Y15614; CAA75704.1; -; Genomic DNA.
DR GO; GO:0003676; P:nucleic acid binding; IEA.
DR GO; GO:0006355; P:regulation of transcription, DNA-dependent; IEA.
DR InterPro; IPR002568; Carla_bd.
DR Pfam; PF01623; Carla_C4; 1.
DR NON TER .93
SQ SEQUENCE 93 AA; 10566 MW; 11BD8D5D69865A75 CRC64;

Query Match 51.6%; Score 47; DB 2; Length 93;
Best Local Similarity 52.9%; Pred. No. 5;
Matches 9; Conservative 4; Mismatches 4; Indels 0; Gaps 0;

QY 2 GGRLSYRRRPFSTGCR 18
|||:|:|:|:|
DB 38 GGRSTYARKRRARSIGR 54

```

```

RESULT 22
O73525_9VIRU
ID O73525_9VIRU PRELIMINARY; PRT; 94 AA.
AC O73525;
DT 01-AUG-1998, integrated into UniProtKB/TrEMBL.
DT 01-AUG-1998, sequence version 1.
DT 07-FEB-2006, entry version 18.
DE 11k protein.
OS Potato virus S.
OC Viruses; ssRNA positive-strand viruses, no DNA stage; Flexiviridae;
OC Carlavirus.
OX NCBI_TaxID=12169;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RC STRAIN=Kobra;
RA Matousek J., Schubert J., Dedic P., Ptacek J.;
RT "A broad variability of pot ato virus S (PVS) revealed by analysis of
RT virus sequences amplified by reverse t transcriptase-polymerase chain
RT reaction.";
RL Can. J. Plant Pathol. 22:22-29(2000).
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CC -----
DR EMBL; Y15625; CAA75721.1; -; Genomic DNA.
DR GO; GO:0003676; P:nucleic acid binding; IEA.
DR GO; GO:0006355; P:regulation of transcription, DNA-dependent; IEA.
DR InterPro; IPR002568; Carla_bd.
DR Pfam; PF01623; Carla_C4; 1.
DR NON TER .94
SQ SEQUENCE 94 AA; 10666 MW; 5236BDFD583C830A CRC64;

Query Match 51.6%; Score 47; DB 2; Length 94;
Best Local Similarity 52.9%; Pred. No. 5;
Matches 9; Conservative 4; Mismatches 4; Indels 0; Gaps 0;

QY 2 GGRLSYRRRPFSTGCR 18
|||:|:|:|:|
DB 38 GGRSTYARKRRARSIGR 54

RESULT 23
Q4A3Q5_9VIRU
ID Q4A3Q5_9VIRU PRELIMINARY; PRT; 94 AA.
AC Q4A3Q5;
DT 13-SEP-2005, integrated into UniProtKB/TrEMBL.
DT 13-SEP-2005, sequence version 1.
DT 07-FEB-2006, entry version 2.
DE 11k protein.
GN Name=11k;
OS Potato virus S.
OC Viruses; ssRNA positive-strand viruses, no DNA stage; Flexiviridae;
OC Carlavirus.
OX NCBI_TaxID=12169;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RC STRAIN=Leona;
RA Matousek J., Schubert J., Ptacek J., Kozlova P., Dedic P.;
RT "Molecular probing of PVS genome by immunocapture RT PCR and by
RT thermodynamic analysis.";
RL Submitted (NOV-2004) to the EMBL/GenBank/DBJ databases.
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CC -----
DR EMBL; AJ863509; CAI06120.1; -; Genomic RNA.
DR GO; GO:0003676; P:nucleic acid binding; IEA.
DR GO; GO:0006355; P:regulation of transcription, DNA-dependent; IEA.
DR NON TER .94
SQ SEQUENCE 94 AA; 10664 MW; A600348D6FCA8C44 CRC64;

Query Match 51.6%; Score 47; DB 2; Length 94;
Best Local Similarity 52.9%; Pred. No. 5;

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Matches 9; Conservative 4; Mismatches 4; Indels 0; Gaps 0;
QY 2 GGRLSYRRRPFSTSTGR 18
DB 38 GGRSTYARKRRARSIGR 54
||||:|:|:|

RESULT 24
Q4U6V1_9VIRU
ID Q4U6V1_9VIRU PRELIMINARY; PRT; 94 AA.
AC Q4U6V1;
DT 05-JUL-2005, integrated into UniProtKB/TrEMBL.
DT 05-JUL-2005, sequence version 1.
DT 07-FEB-2006, entry version 3.
DE 11k protein.
OS Potato virus S.
OC Viruses; ssRNA positive-strand viruses, no DNA stage; Flexiviridae;
OC Carlavirus.
OX NCBI_TaxID=12169;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RC STRAIN=Andean;
RA Bystricka D., Lenz O., Mraz O., Pihrova L., Kmoch S., Sip M.;
RT "Oligonucleotide-based microarray: a new improvement in microarray
detection of plant viruses.";
RL Submitted (APR-2005) to the EMBL/GenBank/DBJ databases.
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CC -----
DR EMBL; DQ000231; AAY33743.1; -; Genomic RNA.
DR GO; GO:0003676; P:nucleic acid binding; IEA.
DR GO; GO:0006355; P:regulation of transcription, DNA-dependent; IEA.
SQ SEQUENCE 94 AA; 10680 MW; 3E31A1FA37C4465A CRC64;

Query Match 51.6%; Score 47; DB 2; Length 94;
Best Local Similarity 52.9%; Pred. No. 5;
Matches 9; Conservative 4; Mismatches 4; Indels 0; Gaps 0;
QY 2 GGRLSYRRRPFSTSTGR 18
DB 38 GGRSTYARKRRARSIGR 54
||||:|:|:|

RESULT 25
Q6R5K2_9VIRU
ID Q6R5K2_9VIRU PRELIMINARY; PRT; 94 AA.
AC Q6R5K2;
DT 05-JUL-2004, integrated into UniProtKB/TrEMBL.
DT 05-JUL-2004, sequence version 1.
DT 07-FEB-2006, entry version 8.
DE 11k protein.
OS Potato virus S.
OC Viruses; ssRNA positive-strand viruses, no DNA stage; Flexiviridae;
OC Carlavirus.
OX NCBI_TaxID=12169;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RC Du Z.Y., Chen J.S.;
RL Submitted (DEC-2003) to the EMBL/GenBank/DBJ databases.
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CC -----
DR EMBL; AY512653; AAS16473.1; -; Genomic RNA.
DR GO; GO:0003676; P:nucleic acid binding; IEA.
DR GO; GO:0006355; P:regulation of transcription, DNA-dependent; IEA.
DR InterPro; IPR002568; Carla_b.
DR Pfam; PF01623; Carla_C4; 1.
SQ SEQUENCE 94 AA; 10708 MW; 9B61A1B3A5FFFD6 CRC64;

Query Match 51.6%; Score 47; DB 2; Length 94;
Best Local Similarity 52.9%; Pred. No. 5;
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Matches 9; Conservative 4; Mismatches 4; Indels 0; Gaps 0;
QY 2 GGRLSYRRRPFSTSTGR 18
DB 38 GGRSTYARKRRARSIGR 54
||||:|:|:|

RESULT 26
Q86541_9VIRU
ID Q86541_9VIRU PRELIMINARY; PRT; 94 AA.
AC Q86541;
DT 01-NOV-1996, integrated into UniProtKB/TrEMBL.
DT 01-NOV-1996, sequence version 1.
DT 07-FEB-2006, entry version 22.
DE 11 kDa protein (Polyprotein).
GN Name=11 kDa protein;
OS Potato virus S.
OC Viruses; ssRNA positive-strand viruses, no DNA stage; Flexiviridae;
OC Carlavirus.
OX NCBI_TaxID=12169;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RX MEDLINE=93033173; PubMed=1413539;
RA Foster G.D., Mills P.R.;
RT "The 3'-nucleotide sequence of an ordinary strain of potato virus S.";
RL Virus Genes 6:213-220(1992).
RN [2]
RP NUCLEOTIDE SEQUENCE.
RC STRAIN=Ordinary;
RA Bystricka D., Lenz O., Mraz O., Pihrova L., Kmoch S., Sip M.;
RT "Oligonucleotide-based microarray: a new improvement in microarray
detection of plant viruses.";
RL Submitted (APR-2005) to the EMBL/GenBank/DBJ databases.
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CC -----
DR EMBL; S45593; AAB23462.1; -; Genomic RNA.
DR EMBL; DQ000232; AAY33744.1; -; Genomic RNA.
DR FIR; B48549; B48549.
DR GO; GO:0003676; P:nucleic acid binding; IEA.
DR GO; GO:0006355; P:regulation of transcription, DNA-dependent; IEA.
DR InterPro; IPR002568; Carla_b.
DR Pfam; PF01623; Carla_C4; 1.
KW Polyprotein.
SQ SEQUENCE 94 AA; 10680 MW; 2241BD8D5D69865A CRC64;

Query Match 51.6%; Score 47; DB 2; Length 94;
Best Local Similarity 52.9%; Pred. No. 5;
Matches 9; Conservative 4; Mismatches 4; Indels 0; Gaps 0;
QY 2 GGRLSYRRRPFSTSTGR 18
DB 38 GGRSTYARKRRARSIGR 54
||||:|:~|:|

RESULT 27
Q3MVD3_9DELT
ID Q3MVD3_9DELT PRELIMINARY; PRT; 391 AA.
AC Q3MVD3;
DT 25-OCT-2005, integrated into UniProtKB/TrEMBL.
DT 25-OCT-2005, sequence version 1.
DT 07-FEB-2006, entry version 3.
DE Alpha-methylacyl-CoA racemase (EC 5.1.99.4).
GN ORFNames=StumDRAFT_3519;
OS Synrophobacter fumeroxidans MFOB.
OC Bacteria; Proteobacteria; Deltaproteobacteria; Synrophobacterales;
OC Synrophobacteraceae; Synrophobacter.
OX NCBI_TaxID=335543;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RC STRAIN=MFOB;
RG US DOE Joint Genome Institute (JGI-PGF);
```



RA Copeland A., Lucas S., Lapidus A., Barry K., Detter J.C., Glavina T.,  
 RT Hammon N., Israni S., Pittluck S., Richardson P.,  
 RT "Sequencing of the draft genome and assembly of Syntriphobacter  
 RL fumaroxidans MPOB.",  
 RL Submitted (JUL-2005) to the EMBL/GenBank/DBJ databases.  
 RN [2]  
 RP NUCLEOTIDE SEQUENCE.  
 RC STRAIN=MPOB;  
 RG US DOE Joint Genome Institute (JGI\_ORNL);  
 RA Larimer F., Land M.;  
 RT "Annotation of the draft genome assembly of Syntriphobacter  
 RL fumaroxidans MPOB.",  
 RL Submitted (JUL-2005) to the EMBL/GenBank/DBJ databases.  
 CC -1- CAUTION: The sequence shown here is derived from an  
 CC EMBL/GenBank/DBJ whole genome shotgun (WGS) entry which is  
 CC preliminary data.  
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 CC -----  
 CC EMBL; AJ2701000109; EAO18902.1; -; Genomic DNA.  
 DR GO; GO:0008111; F:alpha-methylacyl-CoA racemase activity; IEA.  
 DR GO; GO:0016853; F:Isomerase activity; IEA.  
 DR GO; GO:0008152; P:metabolism; IEA.  
 DR InterPro; IPR003673; CA1B\_BA1F.  
 DR Pfam; PF02515; CoA\_transf\_3; 1.  
 KW Isomerases.  
 SQ SEQUENCE 391 AA; 42948 MW; 7CE6207BECFC9F3D CRC64;  
 Query Match 51.6%; Score 47; DB 2; Length 391;  
 Best Local Similarity 64.7%; Pred. No. 26;  
 Matches 11; Conservative 0; Mismatches 6; Indels 0; Gaps 0;  
 QY 1 RGRGLYSRRRPFSTSTG 17  
 DB 145 RSGVLSYSGRAPTWG 161  
 RESULT 28  
 Q55095 CRYNE  
 ID Q55095 CRYNE PRELIMINARY; PRT; 699 AA.  
 AC Q55095;  
 DT 24-MAY-2005, integrated into UniProtKB/TrEMBL.  
 DT 24-MAY-2005, sequence version 1.  
 DT 07-FEB-2006, entry version 3.  
 DE Hypothetical protein.  
 GN ORFNames=CRNF4420;  
 OS Cryptococcus neoformans var. neoformans B-3501A.  
 OC Eukaryota; Fungi; Basidiomycota; Hymenomycetes; Heterobasidiomycetes;  
 OC Tremellomycetidae; Tremellales; Tremellaceae; Filobasidiella.  
 OX NCBI\_TaxID=283643;  
 RN [1]  
 RP NUCLEOTIDE SEQUENCE.  
 RC STRAIN=B-3501A;  
 RA Fung E., Hyman R.W., Rowley D., Bruno D., Miranda M., Fukushima M.,  
 RA Wickes B.L., Fu J., Davis R.W.;  
 RT "Cryptococcus neoformans serotype D sequencing."  
 RL Submitted (JUL-2004) to the EMBL/GenBank/DBJ databases.  
 CC -1- CAUTION: The sequence shown here is derived from an  
 CC EMBL/GenBank/DBJ whole genome shotgun (WGS) entry which is  
 CC preliminary data.  
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 CC -----  
 CC EMBL; AAFY01000032; EAL20116.1; -; Genomic DNA.  
 DR Hypothetical protein.  
 KW SEQUENCE 699 AA; 75973 MW; AFE9D14B9A2254EB CRC64;  
 SQ SEQUENCE 699 AA; 75973 MW; AFE9D14B9A2254EB CRC64;  
 Query Match 51.1%; Score 46.5; DB 2; Length 699;  
 Best Local Similarity 52.2%; Pred. No. 62;  
 Matches 12; Conservative 0; Mismatches 6; Indels 5; Gaps 1;  
 QY 1 RGRGLYSRRRPFSTSTG 18  
 DB 291 RSGRSGYSRSGSISRFGTSNGR 313  
 RESULT 30  
 Q41486 GVIRU  
 ID Q41486 GVIRU PRELIMINARY; PRT; 94 AA.  
 AC Q41486;  
 DT 01-JAN-1998, integrated into UniProtKB/TrEMBL.  
 DT 01-JAN-1998, sequence version 1.  
 DT 07-FEB-2006, entry version 18.  
 DE 11k protein.  
 OS Potato virus S.  
 OC Viruses; ssRNA positive-strand viruses, no DNA stage; Flexiviridae;  
 OC Carlavirus.  
 OX NCBI\_TaxID=12169;  
 RN [1]  
 RP NUCLEOTIDE SEQUENCE.  
 RC STRAIN=S-RB;  
 RA Joung Y.H.;  
 RL Submitted (OCT-1996) to the EMBL/GenBank/DBJ databases.  
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QY 1 RGRGLYSRRRPFSTSTG 18  
 DB 291 RSGRSGYSRSGSISRFGTSNGR 313  
 RESULT 29  
 Q5KFX2 CRYNE  
 ID Q5KFX2 CRYNE PRELIMINARY; PRT; 699 AA.  
 AC Q5KFX2;  
 DT 15-FEB-2005, integrated into UniProtKB/TrEMBL.  
 DT 15-FEB-2005, sequence version 1.  
 DT 07-FEB-2006, entry version 8.  
 DE Hypothetical protein.  
 GN OrderedLocNames=CNF00280;  
 OS Cryptococcus neoformans (Filobasidiella neoformans).  
 OC Eukaryota; Fungi; Basidiomycota; Hymenomycetes; Heterobasidiomycetes;  
 OC Tremellomycetidae; Tremellales; Tremellaceae; Filobasidiella.  
 OX NCBI\_TaxID=5207;  
 RN [1]  
 RP NUCLEOTIDE SEQUENCE [LARGE SCALE GENOMIC DNA].  
 RC STRAIN=JRC21;  
 RC PubMed=15653466; DOI=10.1126/science.1103773;  
 RA Loftus B.J., Fung E., Roncaglia P., Rowley D., Amedeo P., Bruno D.,  
 RA Vamathavan J., Miranda M., Anderson I.J., Fraser J.A., Allen J.E.,  
 RA Bosdet I.E., Brent M.R., Chiu R., Doering T.L., Donlin M.J.,  
 RA D'Souza C.A., Fox D.S., Grinberg V., Fu J., Fukushima M., Haas B.J.,  
 RA Huang J.C., Janbon G., Jones S.J.M., Koo H.L., Krzywinski M.I.,  
 RA Kwon-Chung K.J., Lengeler K.B., Maiti R., Marra M.A., Marra R.E.,  
 RA Mathewson C.A., Mitchell T.G., Perlea R., Riggs P.R., Salzberg S.L.,  
 RA Schein J.E., Shvartsbeyn A., Shin H., Shumway M., Specht C.A.,  
 RA Sun B.B., Tenney A., Utterback T.R., Wickes B.L., Wortman J.R.,  
 RA Wye N.H., Kronstad J.W., Lodge J.K., Heitman J., Davis R.W.,  
 RA Fraser C.M., Hyman R.W.;  
 RT "The genome of the basidiomycetous yeast and human pathogen  
 RT Cryptococcus neoformans".  
 RL Science 307:1321-1324 (2005).  
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 CC -----  
 CC EMBL; AB017346; AWA44148.1; -; Genomic DNA.  
 KW Complete proteome; Hypothetical protein.  
 SQ SEQUENCE 699 AA; 75947 MW; 268A18DBABE2B2A2 CRC64;  
 Query Match 51.1%; Score 46.5; DB 2; Length 699;  
 Best Local Similarity 52.2%; Pred. No. 62;  
 Matches 12; Conservative 0; Mismatches 6; Indels 5; Gaps 1;  
 QY 1 RGRGLYSRRRPFSTSTG 18  
 DB 291 RSGRSGYSRSGSISRFGTSNGR 313  
 RESULT 30  
 Q41486 GVIRU  
 ID Q41486 GVIRU PRELIMINARY; PRT; 94 AA.  
 AC Q41486;  
 DT 01-JAN-1998, integrated into UniProtKB/TrEMBL.  
 DT 01-JAN-1998, sequence version 1.  
 DT 07-FEB-2006, entry version 18.  
 DE 11k protein.  
 OS Potato virus S.  
 OC Viruses; ssRNA positive-strand viruses, no DNA stage; Flexiviridae;  
 OC Carlavirus.  
 OX NCBI\_TaxID=12169;  
 RN [1]  
 RP NUCLEOTIDE SEQUENCE.  
 RC STRAIN=S-RB;  
 RA Joung Y.H.;  
 RL Submitted (OCT-1996) to the EMBL/GenBank/DBJ databases.  
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CC -----
DR EMBL; U74376; AAB65087.1; -; Genomic RNA.
DR GO; GO:0003676; F:nucleic acid binding; IEA.
DR GO; GO:0006355; P:regulation of transcription, DNA-dependent; IEA.
DR InterPro; IPR002568; Carla_bd.
DR Pfam; PF01623; Carla_C4; 1.
SQ SEQUENCE 94 AA; 10650 MW; C8CCEDF10F00A10A CRC64;

Query Match 50.5%; Score 46; DB 2; Length 94;
Best Local Similarity 52.0%; Pred. No. 7.5;
Matches 9; Conservative 3; Mismatches 5; Indels 0; Gaps 0;

Qy 2 CGRLSYSRFRSTSTGR 18
Db 38 GGRSTYGRKRARRSTGR 54

RESULT 31
Q3FAL7_9BURK PRELIMINARY; PRT; 233 AA.
AC Q3FAL7;
DT 08-NOV-2005, integrated into UniProtKB/TrEMBL.
DT 08-NOV-2005, sequence version 1.
DE PIRIN, N-terminal.
DE PIRIN, N-terminal.
GN ORFNames=BambDRAFT_2492;
OS Burkholderia ambifaria AMMD.
OC Bacteria; Proteobacteria; Betaproteobacteria; Burkholderiales;
OC Burkholderiaceae; Burkholderia; Burkholderia cepacia complex.
OX NCBI_TaxID=339670;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RC STRAIN=AMMD;
RG US DOE Joint Genome Institute (JGI-PGP);
RA Copeland A., Lucas S., Lapidus A., Barry K., Detter J.C., Glavina T.,
RA Hammon N., Israni S., Pfluck S., Richardson P.;
RT "Sequencing of the draft genome and assembly of Burkholderia ambifaria
RT AMMD.";
RL Submitted (AUG-2005) to the EMBL/GenBank/DBJ databases.
RN [2]
RP NUCLEOTIDE SEQUENCE.
RC STRAIN=AMMD;
RG US DOE Joint Genome Institute (JGI-ORNL);
RA Larimer F., Land M.;
RT "Annotation of the draft genome assembly of Burkholderia ambifaria
RT AMMD.";
RL Submitted (AUG-2005) to the EMBL/GenBank/DBJ databases.
CC -1- CAUTION: The sequence shown here is derived from an
CC EMBL/GenBank/DBJ whole genome shotgun (WGS) entry which is
CC preliminary data.
CC -----
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CC -----
DR EMBL; AAJL01000006; EAO45746.1; -; Genomic DNA.
DR InterPro; IPR012093; Pirin_N.
DR InterPro; IPR003829; Pirin_N.
DR Pfam; PF02678; Pirin; 1.
DR PIRSF; PIRSF006232; Pirin; 1.
SQ SEQUENCE 233 AA; 25062 MW; 183B8AA579CC51B6 CRC64;

Query Match 50.5%; Score 46; DB 2; Length 233;
Best Local Similarity 50.0%; Pred. No. 21;
Matches 9; Conservative 3; Mismatches 6; Indels 0; Gaps 0;

Qy 1 RGGRLSYSRFRSTSTGR 18
Db 124 RGGRPVGAQRFRADDEKR 141

RESULT 32
O16689_CAEEL PRELIMINARY; PRT; 236 AA.
ID O16689_CAEEL
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AC O16689;
DT 01-JAN-1998, integrated into UniProtKB/TrEMBL.
DT 01-DEC-2001, sequence version 2.
DT 07-FEB-2006, entry version 29.
DE Hypothetical protein.
GN ORFNames=K07E8.3;
OS Caenorhabditis elegans.
OC Eukaryota; Metazoa; Nematoda; Chromadorea; Rhabditida; Rhabditoidea;
OC Rhabditidae; Peloderinae; Caenorhabditis.
OX NCBI_TaxID=6239;
RN [1]
RP NUCLEOTIDE SEQUENCE [LARGE SCALE GENOMIC DNA].
RC STRAIN=Bristol N2;
RX MEDLINE=99069613; PubMed=9851916; DOI=10.1126/science.282.5396.2012;
RG The C. elegans sequencing consortium;
RT "Genome sequence of the nematode C. elegans: a platform for
RT investigating biology.";
RL Science 282:2012-2018(1998).
CC -----
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CC -----
DR EMBL; AF016678; AAB66149.2; -; Genomic DNA.
DR PIR; T32047; T32047.
DR Ensemble; K07E8.3; Caenorhabditis elegans.
DR WormBase; WBGene00019495; K07E8.3.
DR WormPep; K07E8.3; CE29512.
DR GO; GO:0003676; F:nucleic acid binding; IEA.
DR InterPro; IPR012340; OB_NA_bd_sub.
DR InterPro; IPR004365; OB_NA_NA_bd.
DR Pfam; PF01336; tRNA_anti_1.
RW Complete proteome; Hypothetical protein.
SQ SEQUENCE 236 AA; 26938 MW; 693B7ABB3795A6C9 CRC64;

Query Match 50.5%; Score 46; DB 2; Length 236;
Best Local Similarity 47.1%; Pred. No. 22;
Matches 8; Conservative 3; Mismatches 6; Indels 0; Gaps 0;

Qy 1 RGGRLSYSRFRSTSTG 17
Db 74 RGGRVYHDKRYPNRTG 90

RESULT 33
Q7PPF7_ANOGA PRELIMINARY; PRT; 288 AA.
AC Q7PPF7;
DT 15-DEC-2003, integrated into UniProtKB/TrEMBL.
DT 07-DEC-2004, sequence version 2.
DT 07-FEB-2006, entry version 13.
DE ENSANGP0000002270 (Fragment).
GN ORFNames=ENSANG000000019781;
OS Anopheles gambiae str. PEST.
OC Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;
OC Neoptera; Endopterygota; Diptera; Nematocera; Culicidae; Culicidae;
OC Anophelinae; Anopheles.
OX NCBI_TaxID=180454;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RC STRAIN=PEST;
RG The Anopheles gambiae Sequence Committee;
RT "Anopheles gambiae re-annotation.";
RL Submitted (APR-2002) to the EMBL/GenBank/DBJ databases.
RN [2]
RP NUCLEOTIDE SEQUENCE.
RC STRAIN=PEST;
RG The Anopheles gambiae Sequence Committee;
RL Submitted (APR-2004) to the EMBL/GenBank/DBJ databases.
CC -1- CAUTION: The sequence shown here is derived from an
CC EMBL/GenBank/DBJ whole genome shotgun (WGS) entry which is
CC preliminary data.
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DR -----
DR EMBL; AA001008948; EAA10488.3; -; Genomic DNA.
DR GO; GO:0016021; C: integral to membrane; IEA.
DR GO; GO:0016020; C: membrane; IEA.
DR GO; GO:0004872; F: receptor activity; IEA.
DR GO; GO:0001584; F: rhodopsin-like receptor activity; IEA.
DR GO; GO:0007186; F: G-protein coupled receptor protein signaln. .; IEA.
DR GO; GO:0007165; P: signal transduction; IEA.
DR InterPro; IPR000276; GPCR_Rhodopsin.
DR PRINTS; PR00001; 7tm.1; 1.
DR PRINTS; PR00237; GPCR_Rhodopsin.
DR PROSITE; PS00237; G_PROTEIN_RECEP_F1_1; UNKNOWN_1.
DR PROSITE; PS00262; G_PROTEIN_RECEP_F1_2; 1.
KW G-protein coupled receptor; Membrane; Receptor; Transducer;
KW Transmembrane.
FT NON TRP 1
SQ SEQUENCE 288 AA; 31036 MW; 39C256679D378FE7 CRC64;

Query Match 50.0%; Score 45.5; DB 2; Length 288;
Best Local Similarity 47.8%; Pred. No. 33;
Matches 11; Conservative 2; Mismatches 3; Indels 7; Gaps 1;

QY 3 GRLSYRRRPS-----TSGR 18
DB 131 GRLGFRRTFTCTVLPSTGTGK 153

RESULT 34
HSPI_MACRU
ID HSPI_MACRU STANDARD; PRT; 59 AA.
AC P42142;
DT 01-NOV-1995, integrated into UniProtKB/Swiss-Prot.
DT 01-NOV-1995, sequence version 1.
DT 07-FEB-2006, entry version 29.
DE Sperm protamine P1.
GN Name=PRM1;
OS Macropus rufus (Red kangaroo) (Megalania rufa).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Metatheria; Diprotodontia; Macropodidae; Macropus.
OX NCBI_TaxID=9321;
RN [1]
RP NUCLEOTIDE SEQUENCE [GENOMIC DNA].
RC TISSUE=Sperm;
RX MEDLINE=5215351; PubMed=7700877;
RA Retief J.D., Krajewski C., Western M., Winkfein R.J., Dixon G.H.;
RT "Molecular phylogeny and evolution of marsupial protamine P1 genes.";
RL Proc. R. Soc. Lond., B, Biol. Sci. 259:7-14(1995).
CC -1- FUNCTION: Protamines substitute for histones in the chromatin of
CC sperm during the haploid phase of spermatogenesis. They compact
CC sperm DNA into a highly condensed, stable and inactive complex.
CC -1- SUBCELLULAR LOCATION: Nucleus.
CC -1- TISSUE SPECIFICITY: Testis.
CC -1- SIMILARITY: Belongs to the protamine P1 family.
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DR EMBL; L35447; AAA74616.1; -; Genomic DNA.
DR InterPro; IPR000221; Protamine P1.
DR Pfam; PF00260; Protamine P1; 1.
DR PROSITE; PS00048; PROTAMINE_P1; 1.
KW Chromosomal protein; Developmental protein; Differentiation;
KW DNA condensation; DNA-binding; Nuclear protein; Nucleosome core;
KW Spermatogenesis.
FT INIT_MET 0
FT CHAIN 1 59
FT By similarity.
FT Sperm protamine P1.
FT /FTID=PRO_0000191494.
SQ SEQUENCE 59 AA; 8230 MW; 78F1AE592B4B2FA2 CRC64;

Query Match 49.5%; Score 45; DB 1; Length 59;
Best Local Similarity 69.2%; Pred. No. 5;
Matches 9; Conservative 1; Mismatches 3; Indels 0; Gaps 0;

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DR -----
DR EMBL; AA001008948; EAA10488.3; -; Genomic DNA.
DR GO; GO:0016021; C: integral to membrane; IEA.
DR GO; GO:0016020; C: membrane; IEA.
DR GO; GO:0004872; F: receptor activity; IEA.
DR GO; GO:0001584; F: rhodopsin-like receptor activity; IEA.
DR GO; GO:0007186; F: G-protein coupled receptor protein signaln. .; IEA.
DR GO; GO:0007165; P: signal transduction; IEA.
DR InterPro; IPR000276; GPCR_Rhodopsin.
DR PRINTS; PR00001; 7tm.1; 1.
DR PRINTS; PR00237; GPCR_Rhodopsin.
DR PROSITE; PS00237; G_PROTEIN_RECEP_F1_1; UNKNOWN_1.
DR PROSITE; PS00262; G_PROTEIN_RECEP_F1_2; 1.
KW G-protein coupled receptor; Membrane; Receptor; Transducer;
KW Transmembrane.
FT NON TRP 1
SQ SEQUENCE 288 AA; 31036 MW; 39C256679D378FE7 CRC64;

Query Match 50.0%; Score 45.5; DB 2; Length 288;
Best Local Similarity 47.8%; Pred. No. 33;
Matches 11; Conservative 2; Mismatches 3; Indels 7; Gaps 1;

QY 3 GRLSYRRRPS-----TSGR 18
DB 131 GRLGFRRTFTCTVLPSTGTGK 153

RESULT 34
HSPI_MACRU
ID HSPI_MACRU STANDARD; PRT; 59 AA.
AC P42142;
DT 01-NOV-1995, integrated into UniProtKB/Swiss-Prot.
DT 01-NOV-1995, sequence version 1.
DT 07-FEB-2006, entry version 29.
DE Sperm protamine P1.
GN Name=PRM1;
OS Macropus rufus (Red kangaroo) (Megalania rufa).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Metatheria; Diprotodontia; Macropodidae; Macropus.
OX NCBI_TaxID=9321;
RN [1]
RP NUCLEOTIDE SEQUENCE [GENOMIC DNA].
RC TISSUE=Sperm;
RX MEDLINE=5215351; PubMed=7700877;
RA Retief J.D., Krajewski C., Western M., Winkfein R.J., Dixon G.H.;
RT "Molecular phylogeny and evolution of marsupial protamine P1 genes.";
RL Proc. R. Soc. Lond., B, Biol. Sci. 259:7-14(1995).
CC -1- FUNCTION: Protamines substitute for histones in the chromatin of
CC sperm during the haploid phase of spermatogenesis. They compact
CC sperm DNA into a highly condensed, stable and inactive complex.
CC -1- SUBCELLULAR LOCATION: Nucleus.
CC -1- TISSUE SPECIFICITY: Testis.
CC -1- SIMILARITY: Belongs to the protamine P1 family.
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DR EMBL; L35447; AAA74616.1; -; Genomic DNA.
DR InterPro; IPR000221; Protamine P1.
DR Pfam; PF00260; Protamine P1; 1.
DR PROSITE; PS00048; PROTAMINE_P1; 1.
KW Chromosomal protein; Developmental protein; Differentiation;
KW DNA condensation; DNA-binding; Nuclear protein; Nucleosome core;
KW Spermatogenesis.
FT INIT_MET 0
FT CHAIN 1 59
FT By similarity.
FT Sperm protamine P1.
FT /FTID=PRO_0000191494.
SQ SEQUENCE 59 AA; 8230 MW; 78F1AE592B4B2FA2 CRC64;

Query Match 49.5%; Score 45; DB 1; Length 59;
Best Local Similarity 69.2%; Pred. No. 5;
Matches 9; Conservative 1; Mismatches 3; Indels 0; Gaps 0;
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QY 1 RGGRLSYRRRPS 13
DB 41 RGGRRGYRRRYS 53

RESULT 35
HSPI_CAEFU
ID HSPI_CAEFU STANDARD; PRT; 60 AA.
AC P42131;
DT 01-NOV-1995, integrated into UniProtKB/Swiss-Prot.
DT 01-NOV-1995, sequence version 1.
DT 07-FEB-2006, entry version 29.
DE Sperm protamine P1.
GN Name=PRM1;
OS Caenolestes fuliginosus (Shrew opossum).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Metatheria; Paucituberculata; Caenolestidae; Caenolestes.
OX NCBI_TaxID=37696;
RN [1]
RP NUCLEOTIDE SEQUENCE [GENOMIC DNA].
RC TISSUE=Sperm;
RX MEDLINE=5215351; PubMed=7700877;
RA Retief J.D., Krajewski C., Western M., Winkfein R.J., Dixon G.H.;
RT "Molecular phylogeny and evolution of marsupial protamine P1 genes.";
RL Proc. R. Soc. Lond., B, Biol. Sci. 259:7-14(1995).
CC -1- FUNCTION: Protamines substitute for histones in the chromatin of
CC sperm during the haploid phase of spermatogenesis. They compact
CC sperm DNA into a highly condensed, stable and inactive complex.
CC -1- SUBCELLULAR LOCATION: Nucleus.
CC -1- TISSUE SPECIFICITY: Testis.
CC -1- SIMILARITY: Belongs to the protamine P1 family.
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DR EMBL; L35332; AAA74598.1; -; Genomic DNA.
DR InterPro; IPR000221; Protamine P1.
DR Pfam; PF00260; Protamine P1; 1.
DR PROSITE; PS00048; PROTAMINE_P1; 1.
KW Chromosomal protein; Developmental protein; Differentiation;
KW DNA condensation; DNA-binding; Nuclear protein; Nucleosome core;
KW Spermatogenesis.
FT INIT_MET 0
FT CHAIN 1 60
FT By similarity.
FT Sperm protamine P1.
FT /FTID=PRO_0000191452.
SQ SEQUENCE 60 AA; 8514 MW; 7630E63AD33A9B05 CRC64;

Query Match 49.5%; Score 45; DB 1; Length 60;
Best Local Similarity 69.2%; Pred. No. 6.7;
Matches 9; Conservative 1; Mismatches 3; Indels 0; Gaps 0;

QY 1 RGGRLSYRRRPS 13
DB 41 RGGRRGYRRRYS 53

RESULT 36
HSPI_DASHA
ID HSPI_DASHA STANDARD; PRT; 60 AA.
AC P67834; P42133; P42135;
DT 11-OCT-2004, integrated into UniProtKB/Swiss-Prot.
DT 11-OCT-2004, sequence version 1.
DT 07-FEB-2006, entry version 10.
DE Sperm protamine P1.
GN Name=PRM1;
OS Dasyurus hallucatus (Satanellus/northern quoll).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Metatheria; Dasyuromorphia; Dasyuridae; Dasyurus.
OX NCBI_TaxID=9280;
RN [1]
RP NUCLEOTIDE SEQUENCE [GENOMIC DNA].
RC TISSUE=Sperm;
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RX MEDLINE=95215351; PubMed=7700877;
RA Retief J.D., Krajewski C., Westerman M., Winkfein R.J., Dixon G.H.;
RT "Molecular phylogeny and evolution of marsupial protamine P1 genes.";
RL Proc. R. Soc. Lond., B, Biol. Sci. 259:7-14(1995).
CC -!- FUNCTION: Protamines substitute for histones in the chromatin of
CC sperm during the haploid phase of spermatogenesis. They compact
CC sperm DNA into a highly condensed, stable and inactive complex.
CC -!- SUBCELLULAR LOCATION: Nucleus.
CC -!- TISSUE SPECIFICITY: Testis.
CC -!- SIMILARITY: Belongs to the protamine P1 family.
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CC
CC -----
DR EMBL; L35341; AAA56795.1; -; Genomic_DNA.
DR InterPro; IPR000221; Protamine P1.
DR Pfam; PF00260; Protamine P1; 1.
DR PROSITE; PS00048; PROTAMINE_P1; 1.
KW Chromosomal protein; Developmental protein; Differentiation;
KW DNA condensation; DNA-binding; Nuclear protein; Nucleosome core;
KW Spermatogenesis.
FT INIT_MET 0 0 By similarity.
FT CHAIN 1 60 Sperm protamine P1.
FT
FT
SQ SEQUENCE 60 AA; 8246 MW; 615D3D85E7123025 CRC64;
Query Match 49.5%; Score 45; DB 1; Length 60;
Best Local Similarity 69.2%; Pred. No. 6.7;
Matches 9; Conservative 1; Mismatches 3; Indels 0; Gaps 0;
QY 1 RGRRLSYRRRFS 13
DB 42 RGRRGYSRRYS 54

RESULT 37
HSP1_DENGO
ID HSP1_DENGO STANDARD; PRT; 60 AA.
AC P67838; Q9GQJ1;
DT 11-OCT-2004, integrated into UniProtKB/Swiss-Prot.
DT 11-OCT-2004, sequence version 1.
DT 07-FEB-2006, entry version 9.
DE Sperm protamine P1.
GN Name=PRM1;
OS Dendrolegus goodfellowi (Goodfellow's tree kangaroo).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Metatheria; Diprotodontia; Macropodidae; Dendrolagus.
OX NCBI_TaxID=69260;
RN [1]
RP NUCLEOTIDE SEQUENCE [GENOMIC DNA].
RA Burk A., Springer M.S.;
RT "Intergenic relationships among Macropodoidea (Metatheria:
RT Diprotodontia) and the chronicle of kangaroo evolution.";
RL J. Mammal. Evol. 7:213-237(2000).
CC -!- FUNCTION: Protamines substitute for histones in the chromatin of
CC sperm during the haploid phase of spermatogenesis. They compact
CC sperm DNA into a highly condensed, stable and inactive complex.
CC -!- SUBCELLULAR LOCATION: Nucleus.
CC -!- TISSUE SPECIFICITY: Testis.
CC -!- SIMILARITY: Belongs to the protamine P1 family.
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CC
CC -----
DR EMBL; AF187537; AAG27954.1; -; Genomic_DNA.
DR InterPro; IPR000221; Protamine P1.
DR Pfam; PF00260; Protamine P1; 1.
DR PROSITE; PS00048; PROTAMINE_P1; 1.
KW Chromosomal protein; Developmental protein; Differentiation;
KW DNA condensation; DNA-binding; Nuclear protein; Nucleosome core;
KW Spermatogenesis.
FT INIT_MET 0 0 By similarity.
FT CHAIN 1 60 Sperm protamine P1.
FT
FT
SQ SEQUENCE 60 AA; 8246 MW; 615D3D85E7123025 CRC64;
Query Match 49.5%; Score 45; DB 1; Length 60;
Best Local Similarity 69.2%; Pred. No. 6.7;
Matches 9; Conservative 1; Mismatches 3; Indels 0; Gaps 0;
QY 1 RGRRLSYRRRFS 13
DB 42 RGRRGYSRRYS 54

RESULT 38
HSP1_MACPA
ID HSP1_MACPA STANDARD; PRT; 60 AA.
AC P42137;
DT 01-NOV-1995, integrated into UniProtKB/Swiss-Prot.
DT 01-NOV-1995, sequence version 1.
DT 07-FEB-2006, entry version 29.
DE Sperm protamine P1.
GN Name=PRM1;
OS Macropus agilis (Agile wallaby).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Metatheria; Diprotodontia; Macropodidae; Macropus.
OX NCBI_TaxID=9313;
RN [1]
RP NUCLEOTIDE SEQUENCE [GENOMIC DNA].
RC TISSUE=Sperm;
RX MEDLINE=95215351; PubMed=7700877;
RA Retief J.D., Krajewski C., Westerman M., Winkfein R.J., Dixon G.H.;
RT "Molecular phylogeny and evolution of marsupial protamine P1 genes.";
RL Proc. R. Soc. Lond., B, Biol. Sci. 259:7-14(1995).
CC -!- FUNCTION: Protamines substitute for histones in the chromatin of
CC sperm during the haploid phase of spermatogenesis. They compact
CC sperm DNA into a highly condensed, stable and inactive complex.
CC -!- SUBCELLULAR LOCATION: Nucleus.
CC -!- TISSUE SPECIFICITY: Testis.
CC -!- SIMILARITY: Belongs to the protamine P1 family.
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CC
CC -----
DR EMBL; L35451; AAA74615.1; -; Genomic_DNA.
DR InterPro; IPR000221; Protamine P1.
DR Pfam; PF00260; Protamine P1; 1.
DR PROSITE; PS00048; PROTAMINE_P1; 1.
KW Chromosomal protein; Developmental protein; Differentiation;
KW DNA condensation; DNA-binding; Nuclear protein; Nucleosome core;
KW Spermatogenesis.
FT INIT_MET 0 0 By similarity.
FT CHAIN 1 60 Sperm protamine P1.
FT
FT
SQ SEQUENCE 60 AA; 8339 MW; 96255C818921EB85 CRC64;
Query Match 49.5%; Score 45; DB 1; Length 60;
Best Local Similarity 69.2%; Pred. No. 6.7;
Matches 9; Conservative 1; Mismatches 3; Indels 0; Gaps 0;
QY 1 RGRRLSYRRRFS 13
DB 41 RGRRGYSRRYS 53

RESULT 39
HSP1_MACPA
ID HSP1_MACPA STANDARD; PRT; 60 AA.
AC Q9GLQ9;
DT 16-NOV-2001, integrated into UniProtKB/Swiss-Prot.
DT 16-NOV-2001, sequence version 2.
DT 07-FEB-2006, entry version 23.
DE Sperm protamine P1.
GN Name=PRM1;
OS Macropus parryi (Whiptail wallaby).
FT
FT
SQ SEQUENCE 60 AA; 8339 MW; 96255C818921EB85 CRC64;
Query Match 49.5%; Score 45; DB 1; Length 60;
Best Local Similarity 69.2%; Pred. No. 6.7;
Matches 9; Conservative 1; Mismatches 3; Indels 0; Gaps 0;
QY 1 RGRRLSYRRRFS 13
DB 41 RGRRGYSRRYS 53
```

```

KW Chromosomal protein; Developmental protein; Differentiation;
KW DNA condensation; DNA-binding; Nuclear protein; Nucleosome core;
KW Spermatogenesis.
FT INIT MET 0 0 By similarity.
FT CHAIN 1 60 Sperm protamine P1.
/FTID=PRO 0000191514.
SQ SEQUENCE 60 AA; 8325 MW; AD48EFC92BA94B27 CRC64;

Query Match 49.5%; Score 45; DB 1; Length 60;
Best Local Similarity 69.2%; Pred. No. 6.7;
Matches 9; Conservative 1; Mismatches 3; Indels 0;

QY 1 RGRLLSYSRRRFS 13
   ||| |||||
Db 41 RGRRCYSRRRYS 53

Search completed: May 21, 2006, 00:24:02
Job time : 296 secs

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